

OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 22:56:12 ; Search time 9798 Seconds  
(without alignments)  
12210.247 Million cell updates/sec

Title: US-10-015-391A-276  
Perfect score: 3143  
Sequence: 1 gggctgaggcactgagagac.....aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gssl:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | %     |              | DB | ID        | Description        |
|------------|--------|-------|--------------|----|-----------|--------------------|
|            |        | Query | Match Length |    |           |                    |
| 1          | 3005   | 95.6  | 3005         | 3  | CR623694  | CR623694 full-leng |
| 2          | 2927.6 | 93.1  | 3151         | 3  | HSM807023 | BX640891 Homo sapi |
| 3          | 1874   | 59.6  | 2172         | 9  | AY402621  | AY402621 Homo sapi |
| 4          | 1765.4 | 56.2  | 2133         | 9  | AY402622  | AY402622 Pan trogl |
| 5          | 1747.4 | 55.6  | 3206         | 3  | AK077976  | AK077976 Mus muscu |
| 6          | 1701.4 | 54.1  | 3086         | 3  | AK035918  | AK035918 Mus muscu |
| 7          | 1372.2 | 43.7  | 2172         | 9  | AY402623  | AY402623 Mus muscu |
| c 8        | 950.6  | 30.2  | 1108         | 5  | BX367242  | BX367242 BX367242  |

|   |    |       |      |      |   |          |          |           |
|---|----|-------|------|------|---|----------|----------|-----------|
| c | 9  | 926.2 | 29.5 | 1064 | 5 | BX363741 | BX363741 | BX363741  |
| c | 10 | 874.4 | 27.8 | 922  | 5 | BX350606 | BX350606 | BX350606  |
|   | 11 | 849.2 | 27.0 | 934  | 5 | BX384966 | BX384966 | BX384966  |
|   | 12 | 839   | 26.7 | 897  | 5 | BX328255 | BX328255 | BX328255  |
|   | 13 | 827.4 | 26.3 | 974  | 5 | BQ057192 | BQ057192 | AGENCOURT |
|   | 14 | 820.4 | 26.1 | 944  | 5 | BX390196 | BX390196 | BX390196  |
| c | 15 | 779.8 | 24.8 | 797  | 6 | CB243787 | CB243787 | UI-CF-FN0 |
|   | 16 | 775   | 24.7 | 801  | 5 | BX112994 | BX112994 | BX112994  |
|   | 17 | 769.8 | 24.5 | 912  | 5 | BQ883972 | BQ883972 | AGENCOURT |
|   | 18 | 768   | 24.4 | 958  | 5 | BX376660 | BX376660 | BX376660  |
|   | 19 | 757.6 | 24.1 | 892  | 6 | CD107028 | CD107028 | AGENCOURT |
| c | 20 | 756.2 | 24.1 | 819  | 6 | CD631371 | CD631371 | 56050427H |
|   | 21 | 748.6 | 23.8 | 951  | 5 | BQ056228 | BQ056228 | AGENCOURT |
|   | 22 | 696.6 | 22.2 | 775  | 1 | AU122156 | AU122156 | AU122156  |
|   | 23 | 691.2 | 22.0 | 970  | 5 | BQ707628 | BQ707628 | AGENCOURT |
|   | 24 | 681   | 21.7 | 1066 | 4 | BM806752 | BM806752 | AGENCOURT |
| c | 25 | 675.2 | 21.5 | 763  | 6 | CD631373 | CD631373 | 56066030H |
|   | 26 | 674   | 21.4 | 727  | 7 | CN255817 | CN255817 | 170004252 |
|   | 27 | 673   | 21.4 | 960  | 5 | BX367243 | BX367243 | BX367243  |
|   | 28 | 666   | 21.2 | 706  | 6 | CD631372 | CD631372 | 56050427J |
|   | 29 | 664   | 21.1 | 681  | 7 | CV023527 | CV023527 | 490 Full  |
|   | 30 | 661.8 | 21.1 | 666  | 4 | BG684636 | BG684636 | 602635914 |
|   | 31 | 650   | 20.7 | 925  | 5 | BQ937439 | BQ937439 | AGENCOURT |
| c | 32 | 627.4 | 20.0 | 640  | 6 | CA311774 | CA311774 | UI-CF-FN0 |
| c | 33 | 612   | 19.5 | 624  | 4 | BM666780 | BM666780 | UI-E-CL1- |
|   | 34 | 609.8 | 19.4 | 1119 | 4 | BI550650 | BI550650 | 603195823 |
|   | 35 | 608.4 | 19.4 | 803  | 7 | CN539797 | CN539797 | UI-M-HU0- |
|   | 36 | 598.6 | 19.0 | 621  | 2 | AW965845 | AW965845 | EST377918 |
| c | 37 | 598.4 | 19.0 | 634  | 5 | BU632880 | BU632880 | UI-H-FE1- |
| c | 38 | 594   | 18.9 | 618  | 5 | BU686374 | BU686374 | UI-CF-DU1 |
|   | 39 | 590.8 | 18.8 | 740  | 6 | CD631374 | CD631374 | 56066030J |
|   | 40 | 585.2 | 18.6 | 881  | 5 | BQ960065 | BQ960065 | AGENCOURT |
|   | 41 | 579.2 | 18.4 | 720  | 6 | CA315771 | CA315771 | UI-M-FW0- |
|   | 42 | 579   | 18.4 | 580  | 5 | BP346261 | BP346261 | BP346261  |
|   | 43 | 576.2 | 18.3 | 582  | 5 | BP312448 | BP312448 | BP312448  |
|   | 44 | 568.6 | 18.1 | 783  | 7 | CK483764 | CK483764 | AGENCOURT |
|   | 45 | 566.8 | 18.0 | 582  | 5 | BP305311 | BP305311 | BP305311  |
|   | 46 | 565.8 | 18.0 | 571  | 7 | CR554650 | CR554650 | DKFZp4590 |
|   | 47 | 557.8 | 17.7 | 796  | 5 | BU052878 | BU052878 | UI-M-FC0- |
|   | 48 | 554.4 | 17.6 | 718  | 7 | CK837783 | CK837783 | 4063044 B |
|   | 49 | 552.6 | 17.6 | 917  | 6 | CA454892 | CA454892 | AGENCOURT |
|   | 50 | 552.4 | 17.6 | 779  | 4 | BI683727 | BI683727 | 603306287 |
|   | 51 | 551.4 | 17.5 | 695  | 4 | BG685741 | BG685741 | 602637838 |
|   | 52 | 547   | 17.4 | 547  | 4 | BM128651 | BM128651 | if14b09.y |
|   | 53 | 546.6 | 17.4 | 709  | 5 | BQ573544 | BQ573544 | UI-M-FD0- |
|   | 54 | 542.6 | 17.3 | 667  | 4 | BG703963 | BG703963 | 602687061 |
|   | 55 | 542.2 | 17.3 | 784  | 5 | BQ043061 | BQ043061 | UI-M-EG0p |
|   | 56 | 538.6 | 17.1 | 841  | 6 | CB566426 | CB566426 | AGENCOURT |
|   | 57 | 530   | 16.9 | 550  | 5 | BP292524 | BP292524 | BP292524  |
|   | 58 | 528   | 16.8 | 528  | 6 | CA393520 | CA393520 | cs39b03.y |
|   | 59 | 526.2 | 16.7 | 944  | 4 | BI250501 | BI250501 | 602993551 |
|   | 60 | 524.4 | 16.7 | 858  | 7 | CK022938 | CK022938 | AGENCOURT |
| c | 61 | 522.4 | 16.6 | 536  | 5 | BQ356019 | BQ356019 | PM3-HT130 |
|   | 62 | 510.8 | 16.3 | 793  | 4 | BI146386 | BI146386 | 602910749 |
|   | 63 | 510   | 16.2 | 666  | 2 | BE868099 | BE868099 | 601443414 |
|   | 64 | 507.8 | 16.2 | 519  | 7 | CK819350 | CK819350 | if14b09.y |
|   | 65 | 500.2 | 15.9 | 532  | 4 | BM691378 | BM691378 | UI-E-CI1- |

|   |     |       |      |     |   |          |          |             |
|---|-----|-------|------|-----|---|----------|----------|-------------|
|   | 66  | 500.2 | 15.9 | 758 | 4 | BI105301 | BI105301 | 602893591   |
| c | 67  | 498   | 15.8 | 567 | 1 | AU147813 | AU147813 | AU147813    |
|   | 68  | 495.4 | 15.8 | 628 | 7 | CN792080 | CN792080 | 4126901 B   |
|   | 69  | 494   | 15.7 | 598 | 2 | BE588408 | BE588408 | 194035 BA   |
|   | 70  | 486.6 | 15.5 | 788 | 7 | CK481778 | CK481778 | AGENCOURT   |
|   | 71  | 486   | 15.5 | 969 | 4 | BG247839 | BG247839 | 602359548   |
|   | 72  | 481.6 | 15.3 | 632 | 7 | CK625364 | CK625364 | mi32c08.y   |
|   | 73  | 481   | 15.3 | 481 | 4 | BM694992 | BM694992 | UI-E-CL1-   |
| c | 74  | 478.8 | 15.2 | 503 | 1 | AI817099 | AI817099 | wj76h11.x   |
|   | 75  | 478.8 | 15.2 | 810 | 6 | CB587284 | CB587284 | AGENCOURT   |
|   | 76  | 476.8 | 15.2 | 544 | 4 | BI481387 | BI481387 | H2RPE-174   |
|   | 77  | 470.4 | 15.0 | 530 | 1 | AA481246 | AA481246 | aa34h11.r   |
| c | 78  | 469.2 | 14.9 | 562 | 2 | AW836429 | AW836429 | PM3-LT003   |
|   | 79  | 467.8 | 14.9 | 821 | 5 | BQ442696 | BQ442696 | UI-M-EV0-   |
|   | 80  | 465.4 | 14.8 | 806 | 7 | CK481746 | CK481746 | AGENCOURT   |
|   | 81  | 464.6 | 14.8 | 585 | 4 | BI359871 | BI359871 | 384615 MA   |
|   | 82  | 462.6 | 14.7 | 667 | 2 | AW914963 | AW914963 | EST346267   |
|   | 83  | 462.2 | 14.7 | 887 | 4 | BI219079 | BI219079 | 602938695   |
|   | 84  | 461.4 | 14.7 | 672 | 6 | BY747595 | BY747595 | BY747595    |
|   | 85  | 461.2 | 14.7 | 892 | 5 | BQ934892 | BQ934892 | AGENCOURT   |
|   | 86  | 449.6 | 14.3 | 537 | 2 | AW657913 | AW657913 | 93554 MAR   |
|   | 87  | 447   | 14.2 | 872 | 4 | BI150290 | BI150290 | 602915311   |
| c | 88  | 446.4 | 14.2 | 450 | 1 | AI568200 | AI568200 | tn66h01.x   |
|   | 89  | 444   | 14.1 | 822 | 7 | CO565372 | CO565372 | AGENCOURT   |
|   | 90  | 443.8 | 14.1 | 659 | 6 | BY747925 | BY747925 | BY747925    |
| c | 91  | 443.4 | 14.1 | 456 | 5 | BU726485 | BU726485 | UI-E-CI1-   |
| c | 92  | 442.4 | 14.1 | 444 | 5 | BQ356020 | BQ356020 | PM3-HT130   |
| c | 93  | 440.6 | 14.0 | 468 | 5 | BQ356018 | BQ356018 | PM3-HT130   |
|   | 94  | 439.6 | 14.0 | 578 | 4 | BI341318 | BI341318 | 368709 MA   |
| c | 95  | 436.8 | 13.9 | 440 | 1 | AA973640 | AA973640 | oo48c04.s   |
|   | 96  | 435.2 | 13.8 | 579 | 4 | BI360284 | BI360284 | 387146 MA   |
|   | 97  | 432.4 | 13.8 | 621 | 9 | CG591258 | CG591258 | OST245642   |
|   | 98  | 431   | 13.7 | 632 | 7 | CO581119 | CO581119 | ILLUMIGEN   |
|   | 99  | 430.8 | 13.7 | 794 | 2 | BF578994 | BF578994 | 602096109   |
|   | 100 | 427   | 13.6 | 563 | 4 | BM030859 | BM030859 | 495387 MA   |
| c | 101 | 426.8 | 13.6 | 441 | 1 | AA554541 | AA554541 | nl14b01.s   |
|   | 102 | 426.8 | 13.6 | 827 | 7 | CO404310 | CO404310 | AGENCOURT   |
|   | 103 | 425.2 | 13.5 | 443 | 2 | BF882612 | BF882612 | QV3-ET020   |
| c | 104 | 425.2 | 13.5 | 457 | 1 | AI291110 | AI291110 | qml0d09.x   |
|   | 105 | 422.8 | 13.5 | 546 | 2 | BF199358 | BF199358 | 249500 MA   |
|   | 106 | 422.4 | 13.4 | 759 | 4 | BG243769 | BG243769 | 602357081   |
|   | 107 | 418.4 | 13.3 | 576 | 4 | BI345630 | BI345630 | 374508 MA   |
| c | 108 | 415   | 13.2 | 415 | 1 | AI017230 | AI017230 | ou32d12.x   |
|   | 109 | 415   | 13.2 | 536 | 2 | BF199378 | BF199378 | 249524 MA   |
| c | 110 | 414.6 | 13.2 | 454 | 2 | BF882611 | BF882611 | QV3-ET020   |
|   | 111 | 414.6 | 13.2 | 538 | 2 | BF080018 | BF080018 | 230753 MA   |
| c | 112 | 413.6 | 13.2 | 537 | 5 | BX372943 | BX372943 | BX372943    |
|   | 113 | 413   | 13.1 | 583 | 5 | BP315573 | BP315573 | BP315573    |
| c | 114 | 412.6 | 13.1 | 468 | 7 | T34379   | T34379   | EST66750 Hu |
|   | 115 | 412   | 13.1 | 582 | 5 | BP314196 | BP314196 | BP314196    |
|   | 116 | 411   | 13.1 | 581 | 5 | BP314893 | BP314893 | BP314893    |
|   | 117 | 410.8 | 13.1 | 624 | 4 | BM691301 | BM691301 | UI-E-CI1-   |
|   | 118 | 409   | 13.0 | 582 | 5 | BP312657 | BP312657 | BP312657    |
|   | 119 | 409   | 13.0 | 721 | 2 | BF580373 | BF580373 | 602097124   |
|   | 120 | 408   | 13.0 | 473 | 7 | H08023   | H08023   | yl91d06.r1  |
|   | 121 | 406   | 12.9 | 406 | 7 | CR538178 | CR538178 | DKFZp459F   |
|   | 122 | 405   | 12.9 | 583 | 5 | BP314892 | BP314892 | BP314892    |

|       |       |      |      |   |          |          |             |
|-------|-------|------|------|---|----------|----------|-------------|
| 123   | 404.8 | 12.9 | 870  | 2 | BE306403 | BE306403 | 601102295   |
| 124   | 404.6 | 12.9 | 610  | 4 | BG618720 | BG618720 | 602645175   |
| 125   | 403.2 | 12.8 | 1122 | 2 | BF159534 | BF159534 | 601769029   |
| c 126 | 402.6 | 12.8 | 449  | 1 | AI623385 | AI623385 | ts18g03.x   |
| 127   | 401.4 | 12.8 | 581  | 5 | BP357544 | BP357544 | BP357544    |
| 128   | 395.4 | 12.6 | 634  | 1 | AA646591 | AA646591 | ve46d08.r   |
| 129   | 394.8 | 12.6 | 494  | 4 | BM288077 | BM288077 | 528964 MA   |
| 130   | 392.4 | 12.5 | 766  | 7 | CK478839 | CK478839 | AGENCOURT   |
| 131   | 392.2 | 12.5 | 882  | 2 | BE571537 | BE571537 | 601333983   |
| 132   | 392   | 12.5 | 582  | 5 | BP315572 | BP315572 | BP315572    |
| 133   | 391.6 | 12.5 | 555  | 6 | CB613565 | CB613565 | AMGNNUC:N   |
| 134   | 390.6 | 12.4 | 581  | 6 | CB606887 | CB606887 | AMGNNUC:N   |
| 135   | 388.8 | 12.4 | 465  | 2 | BF882607 | BF882607 | QV3-ET020   |
| 136   | 388   | 12.3 | 618  | 6 | CB579294 | CB579294 | AMGNNUC:N   |
| 137   | 387.4 | 12.3 | 544  | 4 | BI961174 | BI961174 | MONO1_7_A   |
| c 138 | 387   | 12.3 | 405  | 1 | AI221749 | AI221749 | qq93f04.x   |
| 139   | 383   | 12.2 | 713  | 6 | BY763638 | BY763638 | BY763638    |
| c 140 | 380.8 | 12.1 | 412  | 1 | AA761091 | AA761091 | ny13g11.s   |
| 141   | 378   | 12.0 | 598  | 1 | AV617761 | AV617761 | AV617761    |
| 142   | 377.4 | 12.0 | 535  | 5 | BQ552175 | BQ552175 | H4013H07-   |
| 143   | 377.2 | 12.0 | 665  | 4 | BI151295 | BI151295 | 602917272   |
| c 144 | 374.4 | 11.9 | 459  | 2 | BF154829 | BF154829 | PM2-BT076   |
| c 145 | 374.4 | 11.9 | 459  | 4 | BG949399 | BG949399 | PM2-BT076   |
| 146   | 372.4 | 11.8 | 582  | 5 | BP314933 | BP314933 | BP314933    |
| 147   | 370.6 | 11.8 | 600  | 6 | CA530364 | CA530364 | 9034-81 M   |
| 148   | 370.2 | 11.8 | 541  | 2 | AW654459 | AW654459 | 103930 MA   |
| c 149 | 369.4 | 11.8 | 464  | 5 | BQ356179 | BQ356179 | PM3-HT130   |
| 150   | 367.4 | 11.7 | 490  | 2 | AW659681 | AW659681 | 97213 MAR   |
| 151   | 367   | 11.7 | 516  | 2 | BF075002 | BF075002 | 223731 MA   |
| c 152 | 366.4 | 11.7 | 369  | 2 | AW593031 | AW593031 | hg07e10.x   |
| 153   | 363.8 | 11.6 | 368  | 1 | AA419534 | AA419534 | zv03c09.r   |
| 154   | 363.4 | 11.6 | 513  | 4 | BM106299 | BM106299 | 509997 MA   |
| 155   | 360.6 | 11.5 | 742  | 6 | CB249229 | CB249229 | UI-M-FC0-   |
| 156   | 356.4 | 11.3 | 583  | 5 | BP357148 | BP357148 | BP357148    |
| 157   | 355   | 11.3 | 529  | 5 | BU698229 | BU698229 | LL2in1365   |
| c 158 | 354.4 | 11.3 | 363  | 1 | AI221756 | AI221756 | qq93f12.x   |
| 159   | 353   | 11.2 | 576  | 4 | BI914790 | BI914790 | 603184176   |
| c 160 | 351.4 | 11.2 | 737  | 7 | CO425778 | CO425778 | UI-M-HU0-   |
| 161   | 348   | 11.1 | 360  | 7 | T19441   | T19441   | f03002s Tes |
| c 162 | 346   | 11.0 | 358  | 1 | AI682007 | AI682007 | tp45g08.x   |
| 163   | 344.8 | 11.0 | 502  | 5 | BU696522 | BU696522 | LL2in1072   |
| 164   | 344.2 | 11.0 | 623  | 2 | BB628588 | BB628588 | BB628588    |
| 165   | 343.6 | 10.9 | 424  | 2 | AW352877 | AW352877 | 35717 MAR   |
| 166   | 340.4 | 10.8 | 552  | 2 | AW655294 | AW655294 | 106095 MA   |
| 167   | 338.6 | 10.8 | 449  | 5 | BQ336149 | BQ336149 | PM0-MT042   |
| 168   | 337.2 | 10.7 | 545  | 2 | AW654538 | AW654538 | 104068 MA   |
| 169   | 334.8 | 10.7 | 479  | 4 | BM088355 | BM088355 | 501805 MA   |
| 170   | 333.2 | 10.6 | 411  | 2 | BE859656 | BE859656 | UI-M-AL0-   |
| 171   | 332.2 | 10.6 | 443  | 2 | AW355069 | AW355069 | 37338 MAR   |
| 172   | 327.4 | 10.4 | 700  | 5 | BM944176 | BM944176 | UI-M-EH0p   |
| c 173 | 326.8 | 10.4 | 330  | 7 | CK819349 | CK819349 | if14b09.x   |
| 174   | 321.8 | 10.2 | 469  | 1 | AJ650325 | AJ650325 | AJ650325    |
| 175   | 321.2 | 10.2 | 445  | 2 | AW481698 | AW481698 | 37332 MAR   |
| 176   | 320.6 | 10.2 | 433  | 2 | AW355070 | AW355070 | 37337 MAR   |
| 177   | 318.6 | 10.1 | 390  | 6 | CB778065 | CB778065 | AMGNNUC:C   |
| 178   | 318.4 | 10.1 | 432  | 2 | BF019645 | BF019645 | ux14b02.y   |
| c 179 | 316.8 | 10.1 | 353  | 2 | AW628784 | AW628784 | hi39e03.x   |



|   |     |       |      |      |   |          |                    |
|---|-----|-------|------|------|---|----------|--------------------|
|   | 180 | 316.2 | 10.1 | 465  | 7 | R81743   | R81743 yj05d01.r1  |
| c | 181 | 315.8 | 10.0 | 469  | 1 | AI141990 | AI141990 ool7g10.x |
|   | 182 | 312.4 | 9.9  | 443  | 4 | BM106612 | BM106612 510531 MA |
| c | 183 | 310.6 | 9.9  | 346  | 5 | BQ335891 | BQ335891 PM3-MT020 |
| c | 184 | 310   | 9.9  | 356  | 2 | AW298440 | AW298440 UI-H-BW0- |
| c | 185 | 308.4 | 9.8  | 310  | 1 | AA687813 | AA687813 nv12e08.s |
| c | 186 | 308   | 9.8  | 456  | 7 | CV374906 | CV374906 PM3-HT130 |
|   | 187 | 302.6 | 9.6  | 514  | 1 | AA959087 | AA959087 ua08f08.r |
|   | 188 | 302   | 9.6  | 388  | 6 | CB779567 | CB779567 AMGNNUC:N |
|   | 189 | 301   | 9.6  | 582  | 5 | BP250593 | BP250593 BP250593  |
|   | 190 | 299.8 | 9.5  | 717  | 5 | BM946956 | BM946956 UI-M-EH0p |
|   | 191 | 298.6 | 9.5  | 583  | 5 | BU694619 | BU694619 LL2in1402 |
|   | 192 | 298.4 | 9.5  | 437  | 2 | BF605420 | BF605420 271789 MA |
|   | 193 | 293.6 | 9.3  | 435  | 6 | BY596404 | BY596404 BY596404  |
|   | 194 | 293.6 | 9.3  | 480  | 6 | CB537061 | CB537061 772134 MA |
|   | 195 | 293.6 | 9.3  | 512  | 1 | AA510439 | AA510439 vg32e04.r |
| c | 196 | 293.2 | 9.3  | 303  | 7 | T19440   | T19440 f03002t Tes |
|   | 197 | 293   | 9.3  | 439  | 4 | BM030747 | BM030747 495245 MA |
|   | 198 | 289.6 | 9.2  | 689  | 1 | AA274712 | AA274712 vc15g11.r |
|   | 199 | 288.8 | 9.2  | 318  | 2 | BE182018 | BE182018 CM1-HT064 |
|   | 200 | 288.2 | 9.2  | 368  | 2 | AW632286 | AW632286 92080 MAR |
|   | 201 | 287.6 | 9.2  | 655  | 2 | BB621440 | BB621440 BB621440  |
|   | 202 | 287.2 | 9.1  | 475  | 4 | BM286849 | BM286849 527060 MA |
|   | 203 | 286.6 | 9.1  | 418  | 6 | CB765926 | CB765926 AMGNNUC:N |
| c | 204 | 286.4 | 9.1  | 298  | 4 | BM662404 | BM662404 UI-E-CI1- |
|   | 205 | 285.8 | 9.1  | 481  | 7 | W13797   | W13797 ma94g12.r1  |
|   | 206 | 285.8 | 9.1  | 514  | 9 | CG646708 | CG646708 OST393408 |
|   | 207 | 285.6 | 9.1  | 354  | 2 | BE155671 | BE155671 PM2-HT035 |
|   | 208 | 284.4 | 9.0  | 286  | 7 | CN255816 | CN255816 170005325 |
|   | 209 | 283.6 | 9.0  | 398  | 2 | BE014053 | BE014053 125627 MA |
|   | 210 | 280.6 | 8.9  | 532  | 1 | AA575453 | AA575453 vl90b06.r |
|   | 211 | 279.4 | 8.9  | 285  | 7 | CR736197 | CR736197 CR736197  |
|   | 212 | 279   | 8.9  | 512  | 2 | BE012711 | BE012711 122368 MA |
| c | 213 | 273.6 | 8.7  | 343  | 7 | R81500   | R81500 yj05d01.s1  |
| c | 214 | 273.4 | 8.7  | 281  | 7 | Z39973   | Z39973 HSC10E102 n |
|   | 215 | 273   | 8.7  | 736  | 2 | BE288736 | BE288736 601093420 |
|   | 216 | 271.4 | 8.6  | 327  | 7 | Z43916   | Z43916 HSC10E101 n |
|   | 217 | 269.4 | 8.6  | 636  | 6 | BY745271 | BY745271 BY745271  |
|   | 218 | 261.6 | 8.3  | 385  | 6 | CB702615 | CB702615 AMGNNUC:S |
|   | 219 | 261.2 | 8.3  | 338  | 1 | AA193482 | AA193482 zr41d02.r |
|   | 220 | 257.4 | 8.2  | 507  | 2 | BE668290 | BE668290 156950 MA |
|   | 221 | 257.2 | 8.2  | 456  | 2 | BB840212 | BB840212 BB840212  |
|   | 222 | 255   | 8.1  | 307  | 7 | T34380   | T34380 EST66751 Hu |
|   | 223 | 253   | 8.0  | 595  | 7 | CN701121 | CN701121 E0445B08- |
|   | 224 | 248.8 | 7.9  | 2480 | 9 | AY407393 | AY407393 Mus muscu |
|   | 225 | 248.6 | 7.9  | 343  | 2 | AW446374 | AW446374 85396 MAR |
|   | 226 | 247.8 | 7.9  | 407  | 5 | BY201059 | BY201059 BY201059  |
|   | 227 | 247.4 | 7.9  | 339  | 7 | CK942886 | CK942886 4066584 B |
|   | 228 | 247.2 | 7.9  | 415  | 5 | BY237094 | BY237094 BY237094  |
|   | 229 | 244   | 7.8  | 731  | 1 | AI116589 | AI116589 ue27f05.y |
| c | 230 | 241.4 | 7.7  | 528  | 1 | AI350408 | AI350408 qt17b12.x |
|   | 231 | 241   | 7.7  | 330  | 2 | AW483617 | AW483617 55275 MAR |
|   | 232 | 240.6 | 7.7  | 3809 | 3 | AK030331 | AK030331 Mus muscu |
|   | 233 | 239   | 7.6  | 2777 | 3 | AK028896 | AK028896 Mus muscu |
|   | 234 | 234.8 | 7.5  | 548  | 5 | BX515711 | BX515711 BX515711  |
|   | 235 | 233.6 | 7.4  | 517  | 2 | BB867776 | BB867776 BB867776  |
|   | 236 | 233.2 | 7.4  | 359  | 5 | BY344631 | BY344631 BY344631  |

|   |     |       |     |      |   |          |          |           |
|---|-----|-------|-----|------|---|----------|----------|-----------|
|   | 237 | 233   | 7.4 | 529  | 1 | AI119178 | AI119178 | ue23g10.y |
| c | 238 | 232.2 | 7.4 | 259  | 1 | AI698802 | AI698802 | wd31b11.x |
|   | 239 | 229.4 | 7.3 | 352  | 5 | BY209243 | BY209243 | BY209243  |
|   | 240 | 229.4 | 7.3 | 353  | 5 | BY194675 | BY194675 | BY194675  |
|   | 241 | 228.2 | 7.3 | 345  | 6 | CB705908 | CB705908 | AMGNNUC:N |
|   | 242 | 227.6 | 7.2 | 2502 | 9 | AY407391 | AY407391 | Homo sapi |
|   | 243 | 226.2 | 7.2 | 359  | 5 | BY192032 | BY192032 | BY192032  |
|   | 244 | 225.8 | 7.2 | 441  | 2 | BB848500 | BB848500 | BB848500  |
|   | 245 | 222.8 | 7.1 | 354  | 5 | BY186467 | BY186467 | BY186467  |
| c | 246 | 222   | 7.1 | 226  | 1 | AA971074 | AA971074 | op70g02.s |
|   | 247 | 220.6 | 7.0 | 399  | 5 | BY258404 | BY258404 | BY258404  |
| c | 248 | 218.4 | 6.9 | 231  | 1 | AA588098 | AA588098 | nm98h03.s |
|   | 249 | 218.4 | 6.9 | 356  | 5 | BY203094 | BY203094 | BY203094  |
| c | 250 | 216.2 | 6.9 | 224  | 1 | AA481169 | AA481169 | aa34h11.s |
|   | 251 | 216.2 | 6.9 | 555  | 7 | CN699228 | CN699228 | E0418E11- |
|   | 252 | 216.2 | 6.9 | 925  | 5 | BQ929233 | BQ929233 | AGENCOURT |
|   | 253 | 215.4 | 6.9 | 787  | 4 | BI665818 | BI665818 | 603289737 |
|   | 254 | 213.4 | 6.8 | 978  | 5 | BQ219389 | BQ219389 | AGENCOURT |
|   | 255 | 213.2 | 6.8 | 766  | 4 | BI330594 | BI330594 | 602981035 |
|   | 256 | 212.8 | 6.8 | 344  | 5 | BY182086 | BY182086 | BY182086  |
|   | 257 | 212.4 | 6.8 | 342  | 5 | BY190812 | BY190812 | BY190812  |
|   | 258 | 212   | 6.7 | 554  | 1 | AL780781 | AL780781 | AL780781  |
|   | 259 | 211   | 6.7 | 3648 | 3 | AK090073 | AK090073 | Mus muscu |
|   | 260 | 210.6 | 6.7 | 360  | 5 | BY203098 | BY203098 | BY203098  |
|   | 261 | 210   | 6.7 | 350  | 9 | CG604636 | CG604636 | OST280536 |
|   | 262 | 202.8 | 6.5 | 906  | 7 | CF548431 | CF548431 | AGENCOURT |
|   | 263 | 201.6 | 6.4 | 361  | 6 | BY780664 | BY780664 | BY780664  |
|   | 264 | 199.4 | 6.3 | 340  | 5 | BY180833 | BY180833 | BY180833  |
|   | 265 | 198   | 6.3 | 904  | 2 | BF134543 | BF134543 | 601784950 |
|   | 266 | 196.8 | 6.3 | 343  | 5 | BY176481 | BY176481 | BY176481  |
|   | 267 | 194.2 | 6.2 | 457  | 5 | BY225325 | BY225325 | BY225325  |
|   | 268 | 192   | 6.1 | 374  | 6 | CB692309 | CB692309 | AMGNNUC:N |
|   | 269 | 191.8 | 6.1 | 398  | 5 | BY284987 | BY284987 | BY284987  |
|   | 270 | 191.6 | 6.1 | 691  | 7 | CF767810 | CF767810 | CES006164 |
|   | 271 | 190.6 | 6.1 | 298  | 2 | BB586510 | BB586510 | BB586510  |
|   | 272 | 190.4 | 6.1 | 380  | 5 | BY265162 | BY265162 | BY265162  |
|   | 273 | 189.8 | 6.0 | 424  | 5 | BY188709 | BY188709 | BY188709  |
|   | 274 | 189   | 6.0 | 386  | 5 | BY231195 | BY231195 | BY231195  |
|   | 275 | 186.6 | 5.9 | 267  | 4 | BM485185 | BM485185 | 539436 MA |
|   | 276 | 185.4 | 5.9 | 2502 | 9 | AY407392 | AY407392 | Pan trogl |
| c | 277 | 184.6 | 5.9 | 588  | 6 | CB469303 | CB469303 | sn05_G02. |
|   | 278 | 181   | 5.8 | 504  | 2 | BE481474 | BE481474 | 166929 BA |
|   | 279 | 179.2 | 5.7 | 838  | 7 | CF374334 | CF374334 | AGENCOURT |
|   | 280 | 176.4 | 5.6 | 416  | 5 | BY183408 | BY183408 | BY183408  |
| c | 281 | 176   | 5.6 | 560  | 6 | CB476226 | CB476226 | jns118_A0 |
|   | 282 | 172.8 | 5.5 | 710  | 6 | CB422627 | CB422627 | 595748 MA |
|   | 283 | 170   | 5.4 | 312  | 5 | BY170795 | BY170795 | BY170795  |
|   | 284 | 169.2 | 5.4 | 782  | 5 | BP684334 | BP684334 | BP684334  |
|   | 285 | 166.8 | 5.3 | 297  | 5 | BY000550 | BY000550 | BY000550  |
|   | 286 | 165.8 | 5.3 | 356  | 5 | BY233307 | BY233307 | BY233307  |
|   | 287 | 163   | 5.2 | 411  | 6 | BY547048 | BY547048 | BY547048  |
|   | 288 | 163   | 5.2 | 437  | 7 | CV312033 | CV312033 | CM0-PT004 |
|   | 289 | 161.4 | 5.1 | 768  | 5 | BM943605 | BM943605 | UI-M-EH0p |
| c | 290 | 160.4 | 5.1 | 299  | 5 | BQ356197 | BQ356197 | PM3-HT130 |
|   | 291 | 158.2 | 5.0 | 724  | 4 | BG716692 | BG716692 | 602678071 |
|   | 292 | 157   | 5.0 | 902  | 5 | BQ933408 | BQ933408 | AGENCOURT |
| c | 293 | 154.8 | 4.9 | 571  | 6 | CB438091 | CB438091 | 686532 MA |

|       |       |     |      |   |          |          |            |      |
|-------|-------|-----|------|---|----------|----------|------------|------|
| 294   | 154.6 | 4.9 | 473  | 4 | BI775884 | BI775884 | 468605     | MA   |
| 295   | 153.8 | 4.9 | 164  | 7 | D45630   | D45630   | HUMGS02826 |      |
| c 296 | 153.8 | 4.9 | 626  | 6 | CB431656 | CB431656 | 607652     | MA   |
| c 297 | 153.6 | 4.9 | 582  | 6 | CB535123 | CB535123 | 768510     | MA   |
| 298   | 153.2 | 4.9 | 863  | 1 | AI323192 | AI323192 | mp55g10.y  |      |
| 299   | 152   | 4.8 | 745  | 5 | BM962964 | BM962964 | UI-M-EQ0-  |      |
| c 300 | 151.6 | 4.8 | 172  | 2 | AW467911 | AW467911 | he28c12.x  |      |
| 301   | 150.2 | 4.8 | 780  | 7 | CN255480 | CN255480 | 170005312  |      |
| 302   | 149.8 | 4.8 | 615  | 1 | AL677440 | AL677440 | AL677440   |      |
| 303   | 149   | 4.7 | 834  | 5 | BQ216757 | BQ216757 | AGENCOURT  |      |
| 304   | 146.4 | 4.7 | 977  | 5 | BX370082 | BX370082 | BX370082   |      |
| 305   | 146   | 4.6 | 211  | 4 | BI345631 | BI345631 | 374509     | MA   |
| 306   | 146   | 4.6 | 886  | 5 | BQ943608 | BQ943608 | AGENCOURT  |      |
| 307   | 145.8 | 4.6 | 448  | 2 | BB847529 | BB847529 | BB847529   |      |
| 308   | 145   | 4.6 | 416  | 2 | AW430454 | AW430454 | 70020      | MAR  |
| 309   | 143.8 | 4.6 | 615  | 6 | CB437039 | CB437039 | 684474     | MA   |
| 310   | 143.6 | 4.6 | 175  | 2 | AW313646 | AW313646 | 9051       | MARC |
| 311   | 141.8 | 4.5 | 1068 | 4 | BM811543 | BM811543 | AGENCOURT  |      |
| 312   | 141.4 | 4.5 | 926  | 5 | BU909663 | BU909663 | AGENCOURT  |      |
| 313   | 141   | 4.5 | 706  | 7 | CN255488 | CN255488 | 170006001  |      |
| 314   | 141   | 4.5 | 728  | 7 | CN255483 | CN255483 | 170005322  |      |
| 315   | 141   | 4.5 | 864  | 4 | BI518922 | BI518922 | 603061844  |      |
| 316   | 140   | 4.5 | 270  | 2 | BB608272 | BB608272 | BB608272   |      |
| 317   | 140   | 4.5 | 568  | 7 | CN255489 | CN255489 | 170005322  |      |
| 318   | 136.8 | 4.4 | 443  | 5 | BY167445 | BY167445 | BY167445   |      |
| 319   | 136.4 | 4.3 | 580  | 2 | BE752387 | BE752387 | 204762     | MA   |
| 320   | 134   | 4.3 | 160  | 7 | CO261051 | CO261051 | 4133142    | B    |
| 321   | 134   | 4.3 | 948  | 5 | BQ685036 | BQ685036 | AGENCOURT  |      |
| 322   | 133   | 4.2 | 770  | 7 | CO248318 | CO248318 | AGENCOURT  |      |
| c 323 | 132.2 | 4.2 | 573  | 2 | AW118237 | AW118237 | xe12b08.x  |      |
| c 324 | 131.4 | 4.2 | 467  | 1 | AV617760 | AV617760 | AV617760   |      |
| 325   | 131.4 | 4.2 | 615  | 5 | BM945001 | BM945001 | UI-M-EH0p  |      |
| 326   | 130.4 | 4.1 | 563  | 6 | CD216221 | CD216221 | pgp2n.pk0  |      |
| 327   | 130.4 | 4.1 | 700  | 1 | AA763586 | AA763586 | vp07g05.r  |      |
| c 328 | 130   | 4.1 | 561  | 4 | BM252112 | BM252112 | BOTL01000  |      |
| 329   | 129.8 | 4.1 | 614  | 4 | BG712158 | BG712158 | pgl1n.pk0  |      |
| 330   | 129.6 | 4.1 | 418  | 2 | BE679181 | BE679181 | dc60b02.y  |      |
| c 331 | 129.6 | 4.1 | 547  | 4 | BM220500 | BM220500 | C0941F04-  |      |
| c 332 | 129.6 | 4.1 | 598  | 2 | BF714461 | BF714461 | mab01a06.  |      |
| 333   | 129.6 | 4.1 | 700  | 6 | BY763889 | BY763889 | BY763889   |      |
| c 334 | 129.6 | 4.1 | 711  | 5 | BP765487 | BP765487 | BP765487   |      |
| c 335 | 129.6 | 4.1 | 773  | 1 | AI132332 | AI132332 | ue23g10.x  |      |
| c 336 | 129.6 | 4.1 | 780  | 7 | CO040927 | CO040927 | UI-M-EV0-  |      |
| 337   | 129.2 | 4.1 | 678  | 6 | CA041134 | CA041134 | ssalshc50  |      |
| 338   | 129.2 | 4.1 | 3763 | 3 | AK088653 | AK088653 | Mus muscu  |      |
| 339   | 128.8 | 4.1 | 708  | 7 | CN789123 | CN789123 | 4123542    | B    |
| 340   | 128.2 | 4.1 | 372  | 6 | BY540732 | BY540732 | BY540732   |      |
| 341   | 128   | 4.1 | 674  | 2 | BB045065 | BB045065 | BB045065   |      |
| 342   | 127.2 | 4.0 | 290  | 2 | AW656129 | AW656129 | 108203     | MA   |
| c 343 | 127   | 4.0 | 601  | 5 | BP768508 | BP768508 | BP768508   |      |
| 344   | 126.8 | 4.0 | 625  | 2 | BE077531 | BE077531 | RC1-BT060  |      |
| 345   | 126.6 | 4.0 | 342  | 1 | AA611491 | AA611491 | vo89a05.r  |      |
| 346   | 126.6 | 4.0 | 403  | 6 | BY540418 | BY540418 | BY540418   |      |
| 347   | 126.2 | 4.0 | 426  | 2 | BB824296 | BB824296 | BB824296   |      |
| 348   | 126.2 | 4.0 | 435  | 5 | BY517409 | BY517409 | BY517409   |      |
| 349   | 125.8 | 4.0 | 593  | 6 | CD216085 | CD216085 | pgp2n.pk0  |      |
| 350   | 125.6 | 4.0 | 387  | 5 | BY504344 | BY504344 | BY504344   |      |

|       |       |     |     |   |          |          |           |
|-------|-------|-----|-----|---|----------|----------|-----------|
| 351   | 125.6 | 4.0 | 410 | 5 | BY510171 | BY510171 | BY510171  |
| 352   | 125.6 | 4.0 | 422 | 5 | BY494879 | BY494879 | BY494879  |
| 353   | 125.4 | 4.0 | 455 | 7 | CN223958 | CN223958 | WLA052D09 |
| 354   | 125.2 | 4.0 | 306 | 2 | AW436384 | AW436384 | 76556 MAR |
| 355   | 125.2 | 4.0 | 344 | 1 | AA611501 | AA611501 | vo89b04.r |
| 356   | 125.2 | 4.0 | 355 | 1 | AA823216 | AA823216 | vw42b01.r |
| 357   | 125.2 | 4.0 | 366 | 2 | BB792067 | BB792067 | BB792067  |
| c 358 | 125.2 | 4.0 | 386 | 5 | BX639014 | BX639014 | BX639014  |
| c 359 | 125.2 | 4.0 | 396 | 2 | BE851923 | BE851923 | uw18f07.x |
| 360   | 125.2 | 4.0 | 404 | 6 | BY575062 | BY575062 | BY575062  |
| 361   | 125.2 | 4.0 | 405 | 6 | BY625364 | BY625364 | BY625364  |
| 362   | 125.2 | 4.0 | 408 | 6 | BY547045 | BY547045 | BY547045  |
| 363   | 125.2 | 4.0 | 409 | 2 | BB743231 | BB743231 | BB743231  |
| 364   | 125.2 | 4.0 | 414 | 6 | BY538798 | BY538798 | BY538798  |
| 365   | 125.2 | 4.0 | 428 | 6 | BY579800 | BY579800 | BY579800  |
| 366   | 125.2 | 4.0 | 434 | 6 | BY551281 | BY551281 | BY551281  |
| 367   | 125.2 | 4.0 | 437 | 6 | BY523338 | BY523338 | BY523338  |
| c 368 | 125.2 | 4.0 | 441 | 2 | AW061291 | AW061291 | UI-M-BH1- |
| 369   | 125.2 | 4.0 | 449 | 6 | BY546162 | BY546162 | BY546162  |
| 370   | 125.2 | 4.0 | 466 | 2 | BB731279 | BB731279 | BB731279  |
| 371   | 125.2 | 4.0 | 469 | 2 | BB824926 | BB824926 | BB824926  |
| 372   | 125.2 | 4.0 | 492 | 2 | AW493316 | AW493316 | UI-M-BH3- |
| c 373 | 125.2 | 4.0 | 507 | 2 | AW060306 | AW060306 | UI-M-BH1- |
| c 374 | 125.2 | 4.0 | 514 | 2 | BF020082 | BF020082 | ux14b02.x |
| c 375 | 125.2 | 4.0 | 516 | 1 | AI098213 | AI098213 | ue27f05.x |
| c 376 | 125.2 | 4.0 | 546 | 1 | AI323581 | AI323581 | mp55g10.x |
| 377   | 125.2 | 4.0 | 910 | 5 | BU552547 | BU552547 | AGENCOURT |
| 378   | 124.8 | 4.0 | 768 | 7 | CN255481 | CN255481 | 170005331 |
| 379   | 124.4 | 4.0 | 372 | 5 | BY236908 | BY236908 | BY236908  |
| 380   | 124.2 | 4.0 | 387 | 5 | BY511124 | BY511124 | BY511124  |
| 381   | 124.2 | 4.0 | 685 | 6 | CA371810 | CA371810 | 652409 NC |
| 382   | 124   | 3.9 | 396 | 6 | BY548006 | BY548006 | BY548006  |
| c 383 | 124   | 3.9 | 446 | 1 | AI606228 | AI606228 | vn98f09.x |
| 384   | 123.8 | 3.9 | 314 | 2 | AW485003 | AW485003 | 63380 MAR |
| 385   | 123.8 | 3.9 | 862 | 5 | BQ224734 | BQ224734 | AGENCOURT |
| 386   | 123.6 | 3.9 | 399 | 6 | BY541776 | BY541776 | BY541776  |
| 387   | 123.6 | 3.9 | 410 | 5 | BY513291 | BY513291 | BY513291  |
| 388   | 123.6 | 3.9 | 433 | 5 | BY498637 | BY498637 | BY498637  |
| 389   | 123.6 | 3.9 | 660 | 2 | BB126942 | BB126942 | BB126942  |
| 390   | 123.6 | 3.9 | 853 | 7 | CR574223 | CR574223 | CR574223  |
| 391   | 123.4 | 3.9 | 319 | 2 | BB317324 | BB317324 | BB317324  |
| 392   | 123.2 | 3.9 | 406 | 5 | BY516094 | BY516094 | BY516094  |
| c 393 | 123.2 | 3.9 | 446 | 5 | BP754487 | BP754487 | BP754487  |
| 394   | 123.2 | 3.9 | 655 | 4 | BJ618310 | BJ618310 | BJ618310  |
| 395   | 123   | 3.9 | 330 | 2 | BB164759 | BB164759 | BB164759  |
| 396   | 123   | 3.9 | 446 | 2 | BB820315 | BB820315 | BB820315  |
| 397   | 122.8 | 3.9 | 236 | 2 | BF776808 | BF776808 | 288536 MA |
| 398   | 122.8 | 3.9 | 851 | 7 | CF243117 | CF243117 | AGENCOURT |
| 399   | 122.8 | 3.9 | 880 | 5 | BU541109 | BU541109 | AGENCOURT |
| 400   | 122.6 | 3.9 | 399 | 6 | BY658194 | BY658194 | BY658194  |
| 401   | 122.6 | 3.9 | 405 | 2 | BB739127 | BB739127 | BB739127  |
| 402   | 122.6 | 3.9 | 414 | 2 | BE849780 | BE849780 | uw18f07.y |
| 403   | 122.6 | 3.9 | 417 | 5 | BY516312 | BY516312 | BY516312  |
| 404   | 122.6 | 3.9 | 432 | 6 | BY525070 | BY525070 | BY525070  |
| 405   | 122.6 | 3.9 | 445 | 2 | BB779387 | BB779387 | BB779387  |
| 406   | 122.4 | 3.9 | 399 | 5 | BY183603 | BY183603 | BY183603  |
| 407   | 122.4 | 3.9 | 401 | 5 | BY507720 | BY507720 | BY507720  |

|       |       |     |     |   |          |          |           |
|-------|-------|-----|-----|---|----------|----------|-----------|
| 408   | 122.2 | 3.9 | 343 | 2 | BB222788 | BB222788 | BB222788  |
| 409   | 122.2 | 3.9 | 415 | 6 | BY646549 | BY646549 | BY646549  |
| 410   | 122.2 | 3.9 | 420 | 6 | BY524914 | BY524914 | BY524914  |
| c 411 | 122.2 | 3.9 | 515 | 4 | BM390926 | BM390926 | UI-R-CN1- |
| 412   | 122   | 3.9 | 347 | 2 | BB113642 | BB113642 | BB113642  |
| 413   | 122   | 3.9 | 402 | 5 | BY507653 | BY507653 | BY507653  |
| 414   | 121.8 | 3.9 | 314 | 1 | AV235779 | AV235779 | AV235779  |
| 415   | 121.8 | 3.9 | 548 | 2 | BF039888 | BF039888 | BP250025A |
| 416   | 121.8 | 3.9 | 932 | 5 | BX369159 | BX369159 | BX369159  |
| 417   | 121.6 | 3.9 | 623 | 4 | BJ095128 | BJ095128 | BJ095128  |
| 418   | 121.6 | 3.9 | 881 | 4 | BG824522 | BG824522 | 602727494 |
| c 419 | 121.4 | 3.9 | 651 | 4 | BM385797 | BM385797 | UI-R-CN1- |
| 420   | 121.2 | 3.9 | 358 | 5 | BY205630 | BY205630 | BY205630  |
| 421   | 121.2 | 3.9 | 872 | 4 | BG831590 | BG831590 | 602765850 |
| c 422 | 121   | 3.8 | 293 | 7 | CO988317 | CO988317 | UMC-pd3en |
| c 423 | 121   | 3.8 | 387 | 2 | BE690913 | BE690913 | uw60d09.x |
| 424   | 120.8 | 3.8 | 336 | 2 | BB219364 | BB219364 | BB219364  |
| 425   | 120.8 | 3.8 | 589 | 4 | BI391274 | BI391274 | pgpln.pk0 |
| 426   | 120.6 | 3.8 | 351 | 2 | BE668250 | BE668250 | 156853 MA |
| c 427 | 120.6 | 3.8 | 431 | 6 | CA945768 | CA945768 | UI-R-FS1- |
| c 428 | 120.6 | 3.8 | 435 | 1 | AI454122 | AI454122 | UI-R-BT0- |
| c 429 | 120.6 | 3.8 | 473 | 2 | AW523699 | AW523699 | UI-R-BO0- |
| c 430 | 120.6 | 3.8 | 552 | 2 | BE110750 | BE110750 | UI-R-BJ1- |
| c 431 | 120.6 | 3.8 | 555 | 5 | BQ190381 | BQ190381 | UI-R-DN1- |
| c 432 | 120.6 | 3.8 | 649 | 6 | CB322846 | CB322846 | UI-R-DY0- |
| 433   | 120.4 | 3.8 | 328 | 2 | BB223967 | BB223967 | BB223967  |
| 434   | 120.4 | 3.8 | 377 | 6 | BY630131 | BY630131 | BY630131  |
| 435   | 120.4 | 3.8 | 424 | 5 | BY378169 | BY378169 | BY378169  |
| c 436 | 120.4 | 3.8 | 528 | 5 | BQ031863 | BQ031863 | UI-1-CF0- |
| c 437 | 120.2 | 3.8 | 381 | 7 | CR468045 | CR468045 | CR468045  |
| 438   | 120.2 | 3.8 | 446 | 1 | AA254731 | AA254731 | mz80h03.r |
| 439   | 120.2 | 3.8 | 486 | 6 | BY591764 | BY591764 | BY591764  |
| c 440 | 120.2 | 3.8 | 656 | 4 | BM251667 | BM251667 | BOTL01000 |
| 441   | 120   | 3.8 | 324 | 2 | BB503600 | BB503600 | BB503600  |
| 442   | 120   | 3.8 | 904 | 5 | BU543096 | BU543096 | AGENCOURT |
| 443   | 119.8 | 3.8 | 317 | 2 | BB828413 | BB828413 | BB828413  |
| 444   | 119.8 | 3.8 | 414 | 5 | BY498892 | BY498892 | BY498892  |
| 445   | 119.4 | 3.8 | 325 | 2 | BB392255 | BB392255 | BB392255  |
| 446   | 119.4 | 3.8 | 333 | 1 | AA755192 | AA755192 | vq62b08.r |
| 447   | 119.4 | 3.8 | 447 | 6 | BY539681 | BY539681 | BY539681  |
| 448   | 119.2 | 3.8 | 329 | 2 | BB321099 | BB321099 | BB321099  |
| 449   | 119.2 | 3.8 | 961 | 5 | BU542955 | BU542955 | AGENCOURT |
| 450   | 119   | 3.8 | 262 | 2 | AW313948 | AW313948 | 9649 MARC |
| 451   | 119   | 3.8 | 262 | 2 | AW477528 | AW477528 | 13351 MAR |
| 452   | 118.6 | 3.8 | 316 | 2 | BB210291 | BB210291 | BB210291  |
| 453   | 118.4 | 3.8 | 422 | 5 | BY509778 | BY509778 | BY509778  |
| 454   | 118.4 | 3.8 | 808 | 5 | BU187281 | BU187281 | AGENCOURT |
| c 455 | 118.2 | 3.8 | 392 | 4 | BI290997 | BI290997 | UI-R-DK0- |
| 456   | 118.2 | 3.8 | 670 | 7 | CK834036 | CK834036 | 4058164 B |
| 457   | 118.2 | 3.8 | 779 | 7 | CF288502 | CF288502 | AGENCOURT |
| 458   | 118   | 3.8 | 373 | 5 | BY017370 | BY017370 | BY017370  |
| c 459 | 118   | 3.8 | 428 | 6 | CB059945 | CB059945 | 4010160 B |
| 460   | 118   | 3.8 | 763 | 5 | BU612234 | BU612234 | UI-M-EW0- |
| 461   | 117.8 | 3.7 | 409 | 5 | BY506868 | BY506868 | BY506868  |
| 462   | 117.6 | 3.7 | 325 | 2 | BB138812 | BB138812 | BB138812  |
| 463   | 117.6 | 3.7 | 329 | 2 | BB560121 | BB560121 | BB560121  |
| 464   | 117.6 | 3.7 | 453 | 6 | CB060019 | CB060019 | 4010021 B |

|   |     |       |     |      |   |          |          |           |
|---|-----|-------|-----|------|---|----------|----------|-----------|
|   | 465 | 117.6 | 3.7 | 654  | 5 | BP754486 | BP754486 | BP754486  |
|   | 466 | 117.4 | 3.7 | 504  | 1 | AA110742 | AA110742 | mp55g10.r |
|   | 467 | 117.4 | 3.7 | 726  | 7 | CK980025 | CK980025 | 4111598 B |
|   | 468 | 117.2 | 3.7 | 336  | 2 | BB165167 | BB165167 | BB165167  |
|   | 469 | 117.2 | 3.7 | 407  | 5 | BY516195 | BY516195 | BY516195  |
|   | 470 | 117   | 3.7 | 149  | 6 | CB062937 | CB062937 | 4013191 B |
|   | 471 | 117   | 3.7 | 315  | 2 | BB269712 | BB269712 | BB269712  |
|   | 472 | 117   | 3.7 | 738  | 1 | AL702888 | AL702888 | DKFZp686D |
|   | 473 | 117   | 3.7 | 917  | 5 | BU916713 | BU916713 | AGENCOURT |
|   | 474 | 116.8 | 3.7 | 322  | 2 | BB220489 | BB220489 | BB220489  |
|   | 475 | 116.6 | 3.7 | 412  | 6 | CB802007 | CB802007 | AMGNNUC:N |
|   | 476 | 116.6 | 3.7 | 426  | 2 | AW767390 | AW767390 | da68e03.y |
|   | 477 | 116.6 | 3.7 | 711  | 7 | CN401142 | CN401142 | 170005328 |
|   | 478 | 116.6 | 3.7 | 933  | 4 | BG424061 | BG424061 | 602448130 |
| c | 479 | 116.2 | 3.7 | 689  | 5 | BX885697 | BX885697 | BX885697  |
|   | 480 | 116   | 3.7 | 413  | 5 | BY516984 | BY516984 | BY516984  |
|   | 481 | 115.8 | 3.7 | 315  | 2 | BB217943 | BB217943 | BB217943  |
|   | 482 | 115.6 | 3.7 | 308  | 2 | BB226784 | BB226784 | BB226784  |
|   | 483 | 115.6 | 3.7 | 459  | 6 | BY596859 | BY596859 | BY596859  |
|   | 484 | 115.4 | 3.7 | 328  | 2 | BB203677 | BB203677 | BB203677  |
|   | 485 | 115   | 3.7 | 653  | 4 | BG423200 | BG423200 | 602450518 |
|   | 486 | 115   | 3.7 | 1045 | 5 | BX458922 | BX458922 | BX458922  |
|   | 487 | 114.8 | 3.7 | 865  | 5 | BQ962412 | BQ962412 | AGENCOURT |
|   | 488 | 114.6 | 3.6 | 413  | 6 | BY577648 | BY577648 | BY577648  |
|   | 489 | 114.4 | 3.6 | 318  | 2 | BB221006 | BB221006 | BB221006  |
|   | 490 | 114.4 | 3.6 | 3226 | 3 | AK042751 | AK042751 | Mus muscu |
|   | 491 | 114.4 | 3.6 | 3329 | 3 | AK082711 | AK082711 | Mus muscu |
|   | 492 | 114   | 3.6 | 268  | 2 | BB594900 | BB594900 | BB594900  |
|   | 493 | 113.8 | 3.6 | 552  | 7 | CN664343 | CN664343 | A0811H09- |
|   | 494 | 113.4 | 3.6 | 408  | 5 | BY159825 | BY159825 | BY159825  |
|   | 495 | 113.4 | 3.6 | 1035 | 5 | BQ944697 | BQ944697 | AGENCOURT |
|   | 496 | 113.2 | 3.6 | 262  | 2 | BB733435 | BB733435 | BB733435  |
|   | 497 | 113.2 | 3.6 | 297  | 2 | BB082267 | BB082267 | BB082267  |
|   | 498 | 113   | 3.6 | 294  | 2 | BB369725 | BB369725 | BB369725  |
|   | 499 | 113   | 3.6 | 311  | 2 | BB319473 | BB319473 | BB319473  |
|   | 500 | 113   | 3.6 | 647  | 4 | BI159977 | BI159977 | 602863854 |
|   | 501 | 112.8 | 3.6 | 286  | 2 | BB180038 | BB180038 | BB180038  |
|   | 502 | 112.8 | 3.6 | 339  | 2 | BB137126 | BB137126 | BB137126  |
|   | 503 | 112.2 | 3.6 | 339  | 2 | BB224502 | BB224502 | BB224502  |
|   | 504 | 112.2 | 3.6 | 341  | 2 | BB224286 | BB224286 | BB224286  |
|   | 505 | 112.2 | 3.6 | 470  | 2 | BB822561 | BB822561 | BB822561  |
|   | 506 | 112   | 3.6 | 298  | 2 | BB360425 | BB360425 | BB360425  |
|   | 507 | 112   | 3.6 | 316  | 2 | BB218778 | BB218778 | BB218778  |
|   | 508 | 112   | 3.6 | 940  | 4 | BG386070 | BG386070 | 602455244 |
|   | 509 | 111.8 | 3.6 | 287  | 2 | BB179402 | BB179402 | BB179402  |
|   | 510 | 111.8 | 3.6 | 395  | 5 | BY019515 | BY019515 | BY019515  |
|   | 511 | 111.8 | 3.6 | 691  | 4 | BG422155 | BG422155 | 602448882 |
|   | 512 | 111.6 | 3.6 | 300  | 2 | BB522135 | BB522135 | BB522135  |
|   | 513 | 111.6 | 3.6 | 307  | 2 | BB116702 | BB116702 | BB116702  |
|   | 514 | 111.4 | 3.5 | 321  | 2 | BB236584 | BB236584 | BB236584  |
|   | 515 | 111.4 | 3.5 | 338  | 2 | BB120467 | BB120467 | BB120467  |
|   | 516 | 111.2 | 3.5 | 286  | 2 | BB222636 | BB222636 | BB222636  |
|   | 517 | 111.2 | 3.5 | 304  | 2 | BB219012 | BB219012 | BB219012  |
|   | 518 | 111.2 | 3.5 | 306  | 1 | AV239830 | AV239830 | AV239830  |
|   | 519 | 111.2 | 3.5 | 678  | 4 | BM495316 | BM495316 | IpcGBr2_2 |
| c | 520 | 111.2 | 3.5 | 738  | 4 | BM414643 | BM414643 | ECC00109  |
|   | 521 | 111   | 3.5 | 277  | 2 | BB324525 | BB324525 | BB324525  |

|   |     |       |     |      |   |          |          |           |
|---|-----|-------|-----|------|---|----------|----------|-----------|
|   | 522 | 110.8 | 3.5 | 295  | 2 | BB511397 | BB511397 | BB511397  |
|   | 523 | 110.6 | 3.5 | 1606 | 2 | BF581604 | BF581604 | 602099944 |
|   | 524 | 110.4 | 3.5 | 788  | 4 | BI161171 | BI161171 | 602865624 |
|   | 525 | 110.2 | 3.5 | 334  | 2 | BB224542 | BB224542 | BB224542  |
|   | 526 | 110   | 3.5 | 288  | 2 | BB346214 | BB346214 | BB346214  |
|   | 527 | 110   | 3.5 | 310  | 2 | BB265127 | BB265127 | BB265127  |
| c | 528 | 110   | 3.5 | 344  | 1 | AI070233 | AI070233 | UI-R-Y0-1 |
|   | 529 | 109.8 | 3.5 | 306  | 2 | BB530000 | BB530000 | BB530000  |
|   | 530 | 109.8 | 3.5 | 487  | 7 | CN367763 | CN367763 | 170005322 |
|   | 531 | 109.6 | 3.5 | 284  | 2 | BB733429 | BB733429 | BB733429  |
|   | 532 | 109.6 | 3.5 | 293  | 2 | BB334189 | BB334189 | BB334189  |
|   | 533 | 109.6 | 3.5 | 452  | 6 | BY588670 | BY588670 | BY588670  |
|   | 534 | 109.4 | 3.5 | 317  | 1 | AV102365 | AV102365 | AV102365  |
|   | 535 | 109.4 | 3.5 | 826  | 5 | BU175920 | BU175920 | AGENCOURT |
|   | 536 | 109.4 | 3.5 | 1132 | 6 | CD504092 | CD504092 | CDA66-A08 |
|   | 537 | 109.2 | 3.5 | 357  | 5 | BY193799 | BY193799 | BY193799  |
|   | 538 | 109   | 3.5 | 110  | 6 | CD631366 | CD631366 | 56027747J |
|   | 539 | 109   | 3.5 | 292  | 2 | BB440274 | BB440274 | BB440274  |
|   | 540 | 109   | 3.5 | 295  | 2 | BB179256 | BB179256 | BB179256  |
|   | 541 | 109   | 3.5 | 298  | 2 | BB257753 | BB257753 | BB257753  |
|   | 542 | 108.8 | 3.5 | 309  | 2 | BB124269 | BB124269 | BB124269  |
|   | 543 | 108.8 | 3.5 | 310  | 2 | BB335680 | BB335680 | BB335680  |
| c | 544 | 108.6 | 3.5 | 457  | 2 | BE686664 | BE686664 | uw03e06.x |
|   | 545 | 108.4 | 3.4 | 292  | 2 | BB173217 | BB173217 | BB173217  |
|   | 546 | 108.4 | 3.4 | 299  | 2 | BB276146 | BB276146 | BB276146  |
|   | 547 | 108.2 | 3.4 | 168  | 2 | AW345212 | AW345212 | 25329 MAR |
|   | 548 | 108.2 | 3.4 | 311  | 2 | BB143870 | BB143870 | BB143870  |
|   | 549 | 108.2 | 3.4 | 910  | 4 | BI161349 | BI161349 | 602865754 |
|   | 550 | 108   | 3.4 | 290  | 2 | BB278479 | BB278479 | BB278479  |
|   | 551 | 108   | 3.4 | 303  | 2 | BB217218 | BB217218 | BB217218  |
|   | 552 | 108   | 3.4 | 949  | 5 | BU541977 | BU541977 | AGENCOURT |
|   | 553 | 108   | 3.4 | 3137 | 3 | BC051979 | BC051979 | Mus muscu |
|   | 554 | 108   | 3.4 | 3907 | 3 | AK031131 | AK031131 | Mus muscu |
| c | 555 | 107.8 | 3.4 | 557  | 1 | AU147993 | AU147993 | AU147993  |
|   | 556 | 107.6 | 3.4 | 689  | 7 | CO434547 | CO434547 | UI-M-HX0- |
|   | 557 | 107.6 | 3.4 | 1141 | 6 | CA975355 | CA975355 | AGENCOURT |
|   | 558 | 107.4 | 3.4 | 289  | 2 | BB007231 | BB007231 | BB007231  |
|   | 559 | 107.4 | 3.4 | 305  | 2 | BB500334 | BB500334 | BB500334  |
| c | 560 | 107.4 | 3.4 | 436  | 1 | AA913136 | AA913136 | oi17h07.s |
|   | 561 | 107.4 | 3.4 | 569  | 7 | CO258909 | CO258909 | 4130136 B |
| c | 562 | 107.4 | 3.4 | 734  | 5 | BX674351 | BX674351 | BX674351  |
|   | 563 | 107.2 | 3.4 | 312  | 2 | BB445664 | BB445664 | BB445664  |
|   | 564 | 107   | 3.4 | 284  | 2 | BB507939 | BB507939 | BB507939  |
|   | 565 | 106.8 | 3.4 | 289  | 2 | BB496529 | BB496529 | BB496529  |
|   | 566 | 106.8 | 3.4 | 290  | 2 | BB368263 | BB368263 | BB368263  |
|   | 567 | 106.8 | 3.4 | 292  | 2 | BB354765 | BB354765 | BB354765  |
|   | 568 | 106.8 | 3.4 | 304  | 2 | BB336700 | BB336700 | BB336700  |
|   | 569 | 106.8 | 3.4 | 328  | 2 | BB220954 | BB220954 | BB220954  |
|   | 570 | 106.6 | 3.4 | 686  | 4 | BG469296 | BG469296 | 602533135 |
|   | 571 | 106.4 | 3.4 | 279  | 2 | BB371226 | BB371226 | BB371226  |
|   | 572 | 106.4 | 3.4 | 286  | 2 | BB555504 | BB555504 | BB555504  |
|   | 573 | 106.4 | 3.4 | 294  | 1 | AV051876 | AV051876 | AV051876  |
|   | 574 | 106.4 | 3.4 | 336  | 2 | AW226731 | AW226731 | um60b09.y |
| c | 575 | 106.4 | 3.4 | 488  | 4 | BM151697 | BM151697 | TCBAP1E10 |
|   | 576 | 106.2 | 3.4 | 281  | 2 | BB346087 | BB346087 | BB346087  |
|   | 577 | 106.2 | 3.4 | 725  | 7 | CN429157 | CN429157 | 170004252 |
|   | 578 | 106   | 3.4 | 306  | 2 | BB262651 | BB262651 | BB262651  |

|       |       |     |      |   |          |          |           |
|-------|-------|-----|------|---|----------|----------|-----------|
| 579   | 106   | 3.4 | 318  | 2 | BB243620 | BB243620 | BB243620  |
| 580   | 105.8 | 3.4 | 272  | 2 | BB552255 | BB552255 | BB552255  |
| 581   | 105.8 | 3.4 | 283  | 2 | BB128450 | BB128450 | BB128450  |
| 582   | 105.8 | 3.4 | 292  | 2 | BB500569 | BB500569 | BB500569  |
| 583   | 105.8 | 3.4 | 976  | 5 | BQ944147 | BQ944147 | AGENCOURT |
| 584   | 105.6 | 3.4 | 281  | 2 | BB348185 | BB348185 | BB348185  |
| 585   | 105.6 | 3.4 | 811  | 6 | CD653578 | CD653578 | AGENCOURT |
| 586   | 105.6 | 3.4 | 824  | 4 | BM047429 | BM047429 | 603628715 |
| 587   | 105.6 | 3.4 | 900  | 4 | BG326356 | BG326356 | 602425281 |
| 588   | 105.4 | 3.4 | 363  | 6 | CD631362 | CD631362 | 56027755J |
| c 589 | 105.4 | 3.4 | 603  | 7 | CK849657 | CK849657 | 972704 BA |
| c 590 | 105.4 | 3.4 | 742  | 5 | BX910552 | BX910552 | BX910552  |
| 591   | 105.2 | 3.3 | 287  | 2 | BB325091 | BB325091 | BB325091  |
| 592   | 105   | 3.3 | 394  | 6 | CB776364 | CB776364 | AMGNNUC:N |
| 593   | 105   | 3.3 | 860  | 5 | BQ230111 | BQ230111 | AGENCOURT |
| 594   | 105   | 3.3 | 924  | 4 | BG326746 | BG326746 | 602425623 |
| 595   | 105   | 3.3 | 963  | 5 | BU552403 | BU552403 | AGENCOURT |
| 596   | 105   | 3.3 | 1024 | 2 | BE910319 | BE910319 | 601503675 |
| 597   | 104.8 | 3.3 | 262  | 1 | AV241169 | AV241169 | AV241169  |
| 598   | 104.8 | 3.3 | 306  | 2 | BB500200 | BB500200 | BB500200  |
| 599   | 104.8 | 3.3 | 414  | 2 | BB826095 | BB826095 | BB826095  |
| 600   | 104.8 | 3.3 | 795  | 6 | CB245479 | CB245479 | UI-M-FY0- |
| 601   | 104.8 | 3.3 | 911  | 5 | BU501900 | BU501900 | AGENCOURT |
| 602   | 104.8 | 3.3 | 919  | 5 | BU173969 | BU173969 | AGENCOURT |
| 603   | 104.6 | 3.3 | 282  | 2 | BB532703 | BB532703 | BB532703  |
| 604   | 104.6 | 3.3 | 309  | 2 | BB499049 | BB499049 | BB499049  |
| 605   | 104.2 | 3.3 | 310  | 2 | BB236046 | BB236046 | BB236046  |
| 606   | 104.2 | 3.3 | 328  | 2 | BB114323 | BB114323 | BB114323  |
| 607   | 104.2 | 3.3 | 414  | 6 | BY578439 | BY578439 | BY578439  |
| 608   | 104.2 | 3.3 | 897  | 5 | BQ219988 | BQ219988 | AGENCOURT |
| 609   | 104.2 | 3.3 | 927  | 4 | BG831583 | BG831583 | 602765840 |
| 610   | 104   | 3.3 | 266  | 2 | BB716868 | BB716868 | BB716868  |
| 611   | 104   | 3.3 | 283  | 2 | BB528644 | BB528644 | BB528644  |
| 612   | 104   | 3.3 | 288  | 2 | BB342818 | BB342818 | BB342818  |
| 613   | 104   | 3.3 | 2855 | 3 | AK047067 | AK047067 | Mus muscu |
| 614   | 103.8 | 3.3 | 298  | 2 | BB283107 | BB283107 | BB283107  |
| 615   | 103.8 | 3.3 | 879  | 4 | BG831929 | BG831929 | 602765589 |
| 616   | 103.6 | 3.3 | 297  | 2 | BB217129 | BB217129 | BB217129  |
| 617   | 103.6 | 3.3 | 307  | 2 | BB500311 | BB500311 | BB500311  |
| 618   | 103.6 | 3.3 | 311  | 2 | BB533042 | BB533042 | BB533042  |
| 619   | 103.6 | 3.3 | 315  | 2 | BB122455 | BB122455 | BB122455  |
| 620   | 103.6 | 3.3 | 464  | 2 | BB796655 | BB796655 | BB796655  |
| 621   | 103.4 | 3.3 | 314  | 2 | BB239048 | BB239048 | BB239048  |
| 622   | 103.2 | 3.3 | 233  | 2 | BB510804 | BB510804 | BB510804  |
| 623   | 103.2 | 3.3 | 286  | 2 | BB178968 | BB178968 | BB178968  |
| 624   | 103.2 | 3.3 | 467  | 6 | BY556536 | BY556536 | BY556536  |
| 625   | 103.2 | 3.3 | 583  | 4 | BM488072 | BM488072 | pgm2n.pk0 |
| 626   | 103.2 | 3.3 | 868  | 1 | AU140366 | AU140366 | AU140366  |
| 627   | 103   | 3.3 | 282  | 2 | BB310767 | BB310767 | BB310767  |
| 628   | 103   | 3.3 | 619  | 1 | AL118624 | AL118624 | DKFZp761F |
| 629   | 102.8 | 3.3 | 269  | 2 | BB313946 | BB313946 | BB313946  |
| 630   | 102.6 | 3.3 | 271  | 2 | BB216188 | BB216188 | BB216188  |
| 631   | 102.6 | 3.3 | 579  | 5 | BP375801 | BP375801 | BP375801  |
| 632   | 102.6 | 3.3 | 869  | 5 | BM947242 | BM947242 | UI-M-EH0p |
| 633   | 102.6 | 3.3 | 977  | 5 | BU520216 | BU520216 | AGENCOURT |
| 634   | 102.4 | 3.3 | 281  | 2 | BB129002 | BB129002 | BB129002  |
| 635   | 102.2 | 3.3 | 268  | 2 | BB216101 | BB216101 | BB216101  |



|   |     |       |     |      |   |          |          |           |
|---|-----|-------|-----|------|---|----------|----------|-----------|
|   | 636 | 102.2 | 3.3 | 271  | 2 | BB555572 | BB555572 | BB555572  |
|   | 637 | 102.2 | 3.3 | 285  | 2 | BB324617 | BB324617 | BB324617  |
|   | 638 | 102.2 | 3.3 | 342  | 2 | BB223376 | BB223376 | BB223376  |
|   | 639 | 102.2 | 3.3 | 644  | 1 | AL803713 | AL803713 | AL803713  |
|   | 640 | 102.2 | 3.3 | 659  | 7 | CN695559 | CN695559 | E0366G09- |
| c | 641 | 102   | 3.2 | 331  | 1 | AI228417 | AI228417 | EST225112 |
|   | 642 | 102   | 3.2 | 426  | 5 | BY376368 | BY376368 | BY376368  |
| c | 643 | 102   | 3.2 | 654  | 6 | CB420254 | CB420254 | 593189 MA |
|   | 644 | 102   | 3.2 | 6875 | 3 | BC032619 | BC032619 | Homo sapi |
|   | 645 | 101.8 | 3.2 | 222  | 2 | BB150791 | BB150791 | BB150791  |
| c | 646 | 101.8 | 3.2 | 353  | 8 | BZ845553 | BZ845553 | CH240_213 |
| c | 647 | 101.8 | 3.2 | 538  | 8 | AQ434948 | AQ434948 | HS_5126_B |
|   | 648 | 101.8 | 3.2 | 779  | 5 | BX396978 | BX396978 | BX396978  |
|   | 649 | 101.8 | 3.2 | 1002 | 5 | BQ068313 | BQ068313 | AGENCOURT |
|   | 650 | 101.6 | 3.2 | 315  | 2 | BB116770 | BB116770 | BB116770  |
| c | 651 | 101.6 | 3.2 | 537  | 2 | BE349814 | BE349814 | hq43e01.x |
|   | 652 | 101.2 | 3.2 | 317  | 2 | BB213717 | BB213717 | BB213717  |
|   | 653 | 101   | 3.2 | 254  | 2 | BB172165 | BB172165 | BB172165  |
|   | 654 | 101   | 3.2 | 2719 | 3 | AK035993 | AK035993 | Mus muscu |
|   | 655 | 100.8 | 3.2 | 400  | 6 | BY555199 | BY555199 | BY555199  |
| c | 656 | 100.8 | 3.2 | 492  | 1 | AA023538 | AA023538 | mh75d07.r |
|   | 657 | 100.8 | 3.2 | 622  | 6 | CD349441 | CD349441 | UI-M-FY0- |
|   | 658 | 100.6 | 3.2 | 505  | 4 | BI898654 | BI898654 | 479668 MA |
|   | 659 | 100.6 | 3.2 | 651  | 4 | BM491746 | BM491746 | pqp2n.pk0 |
|   | 660 | 100.4 | 3.2 | 285  | 2 | BB177820 | BB177820 | BB177820  |
|   | 661 | 100.2 | 3.2 | 699  | 4 | BG830948 | BG830948 | 602766844 |
|   | 662 | 100.2 | 3.2 | 861  | 7 | CO735048 | CO735048 | SlLE04c10 |
|   | 663 | 100   | 3.2 | 224  | 2 | BB499666 | BB499666 | BB499666  |
|   | 664 | 100   | 3.2 | 286  | 2 | BB110106 | BB110106 | BB110106  |
|   | 665 | 100   | 3.2 | 316  | 2 | BB145363 | BB145363 | BB145363  |
| c | 666 | 100   | 3.2 | 582  | 2 | BF400607 | BF400607 | UI-R-CA0- |
|   | 667 | 100   | 3.2 | 786  | 7 | CK365293 | CK365293 | AGENCOURT |
|   | 668 | 99.8  | 3.2 | 313  | 2 | BB218103 | BB218103 | BB218103  |
|   | 669 | 99.8  | 3.2 | 594  | 7 | CN528682 | CN528682 | UI-M-HQ0- |
|   | 670 | 99.8  | 3.2 | 910  | 4 | BG470201 | BG470201 | 602533710 |
|   | 671 | 99.8  | 3.2 | 3921 | 3 | AK084922 | AK084922 | Mus muscu |
|   | 672 | 99.8  | 3.2 | 4374 | 3 | AK031307 | AK031307 | Mus muscu |
| c | 673 | 99.6  | 3.2 | 278  | 6 | CD631370 | CD631370 | 56027863J |
| c | 674 | 99.6  | 3.2 | 703  | 1 | AU170734 | AU170734 | AU170734  |
|   | 675 | 99.6  | 3.2 | 844  | 7 | CO735027 | CO735027 | SlLE04c10 |
|   | 676 | 99.6  | 3.2 | 880  | 5 | BU186709 | BU186709 | AGENCOURT |
|   | 677 | 99.4  | 3.2 | 286  | 2 | BB333313 | BB333313 | BB333313  |
|   | 678 | 99.4  | 3.2 | 772  | 4 | BG829652 | BG829652 | 602764012 |
|   | 679 | 99.2  | 3.2 | 275  | 2 | BB227524 | BB227524 | BB227524  |
|   | 680 | 99.2  | 3.2 | 326  | 2 | BB559836 | BB559836 | BB559836  |
|   | 681 | 99    | 3.1 | 239  | 1 | AV229642 | AV229642 | AV229642  |
|   | 682 | 99    | 3.1 | 264  | 1 | AV238667 | AV238667 | AV238667  |
|   | 683 | 99    | 3.1 | 316  | 2 | BB532106 | BB532106 | BB532106  |
| c | 684 | 99    | 3.1 | 319  | 4 | BG377549 | BG377549 | UI-R-CU0- |
|   | 685 | 98.6  | 3.1 | 121  | 1 | AI264258 | AI264258 | qk20b04.x |
|   | 686 | 98.6  | 3.1 | 278  | 2 | BB176510 | BB176510 | BB176510  |
|   | 687 | 98.6  | 3.1 | 317  | 1 | AL655823 | AL655823 | AL655823  |
|   | 688 | 98.4  | 3.1 | 100  | 4 | BI002468 | BI002468 | MR3-HN015 |
|   | 689 | 98.4  | 3.1 | 228  | 2 | BB150964 | BB150964 | BB150964  |
|   | 690 | 98.4  | 3.1 | 288  | 2 | BB455324 | BB455324 | BB455324  |
|   | 691 | 98.4  | 3.1 | 320  | 2 | BB242404 | BB242404 | BB242404  |
|   | 692 | 98.2  | 3.1 | 278  | 1 | AV313234 | AV313234 | AV313234  |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 693   | 98.2 | 3.1 | 308  | 2 | BB263999 | BB263999 | BB263999  |
| 694   | 98.2 | 3.1 | 668  | 6 | BY746861 | BY746861 | BY746861  |
| 695   | 98.2 | 3.1 | 4476 | 3 | AK052232 | AK052232 | Mus muscu |
| 696   | 98   | 3.1 | 235  | 2 | BB716819 | BB716819 | BB716819  |
| 697   | 98   | 3.1 | 280  | 2 | BB535881 | BB535881 | BB535881  |
| 698   | 97.6 | 3.1 | 203  | 4 | BM105287 | BM105287 | 508710 MA |
| 699   | 97.6 | 3.1 | 369  | 5 | BY020398 | BY020398 | BY020398  |
| 700   | 97.4 | 3.1 | 705  | 2 | BE294211 | BE294211 | 601172744 |
| 701   | 97.2 | 3.1 | 256  | 2 | BB425457 | BB425457 | BB425457  |
| 702   | 97.2 | 3.1 | 281  | 1 | AV235738 | AV235738 | AV235738  |
| 703   | 97.2 | 3.1 | 640  | 7 | CN460578 | CN460578 | UI-M-HB0- |
| 704   | 97.2 | 3.1 | 704  | 6 | BY741417 | BY741417 | BY741417  |
| 705   | 96.8 | 3.1 | 223  | 1 | AV229388 | AV229388 | AV229388  |
| 706   | 96.8 | 3.1 | 225  | 2 | BB323996 | BB323996 | BB323996  |
| 707   | 96.8 | 3.1 | 236  | 2 | BB019685 | BB019685 | BB019685  |
| 708   | 96.8 | 3.1 | 242  | 2 | BB554948 | BB554948 | BB554948  |
| 709   | 96.8 | 3.1 | 273  | 2 | BB010623 | BB010623 | BB010623  |
| 710   | 96.8 | 3.1 | 286  | 2 | BB309932 | BB309932 | BB309932  |
| 711   | 96.8 | 3.1 | 496  | 7 | CK390327 | CK390327 | K0817F12- |
| 712   | 96.8 | 3.1 | 815  | 4 | BG386811 | BG386811 | 602455071 |
| 713   | 96.8 | 3.1 | 986  | 4 | BG746534 | BG746534 | 602703833 |
| 714   | 96.8 | 3.1 | 1394 | 5 | BM926974 | BM926974 | AGENCOURT |
| 715   | 96.6 | 3.1 | 234  | 2 | BB357534 | BB357534 | BB357534  |
| 716   | 96.6 | 3.1 | 340  | 5 | BY353322 | BY353322 | BY353322  |
| 717   | 96.6 | 3.1 | 342  | 2 | BB241607 | BB241607 | BB241607  |
| 718   | 96.6 | 3.1 | 352  | 5 | BY177856 | BY177856 | BY177856  |
| 719   | 96.6 | 3.1 | 396  | 5 | BY201883 | BY201883 | BY201883  |
| 720   | 96.6 | 3.1 | 795  | 7 | CO571948 | CO571948 | AGENCOURT |
| 721   | 96.4 | 3.1 | 721  | 6 | CA324424 | CA324424 | UI-M-FY0- |
| 722   | 96.4 | 3.1 | 779  | 6 | CA316005 | CA316005 | UI-M-FW0- |
| c 723 | 96.2 | 3.1 | 297  | 1 | AI112352 | AI112352 | UI-R-Y0-m |
| c 724 | 96.2 | 3.1 | 297  | 1 | AI576402 | AI576402 | UI-R-Y0-v |
| 725   | 96.2 | 3.1 | 333  | 1 | AV006222 | AV006222 | AV006222  |
| 726   | 96   | 3.1 | 400  | 5 | BY158515 | BY158515 | BY158515  |
| 727   | 96   | 3.1 | 917  | 4 | BG324311 | BG324311 | 602423309 |
| 728   | 95.8 | 3.0 | 586  | 2 | BF041445 | BF041445 | BP250015B |
| 729   | 95.8 | 3.0 | 673  | 5 | BM951984 | BM951984 | UI-M-EH0- |
| c 730 | 95.8 | 3.0 | 710  | 7 | CK979615 | CK979615 | 4111214 B |
| 731   | 95.4 | 3.0 | 178  | 2 | BF774071 | BF774071 | 283623 MA |
| 732   | 95.4 | 3.0 | 178  | 2 | BF774072 | BF774072 | 283624 MA |
| 733   | 95.4 | 3.0 | 222  | 2 | BB052672 | BB052672 | BB052672  |
| 734   | 95.4 | 3.0 | 238  | 2 | BB034746 | BB034746 | BB034746  |
| 735   | 95.4 | 3.0 | 261  | 2 | BB594935 | BB594935 | BB594935  |
| 736   | 95.4 | 3.0 | 278  | 2 | BB173822 | BB173822 | BB173822  |
| 737   | 95.4 | 3.0 | 281  | 2 | BB108075 | BB108075 | BB108075  |
| 738   | 95.4 | 3.0 | 436  | 5 | BY487960 | BY487960 | BY487960  |
| 739   | 95.2 | 3.0 | 227  | 2 | BB501238 | BB501238 | BB501238  |
| 740   | 95.2 | 3.0 | 243  | 1 | AV232151 | AV232151 | AV232151  |
| 741   | 95.2 | 3.0 | 246  | 2 | BB301620 | BB301620 | BB301620  |
| 742   | 95.2 | 3.0 | 297  | 2 | BB135944 | BB135944 | BB135944  |
| 743   | 95.2 | 3.0 | 325  | 2 | BB218380 | BB218380 | BB218380  |
| c 744 | 95.2 | 3.0 | 434  | 4 | BM193462 | BM193462 | TCBAP1Q13 |
| 745   | 95.2 | 3.0 | 490  | 1 | AI365650 | AI365650 | ap20h08.x |
| 746   | 95   | 3.0 | 380  | 5 | BY165728 | BY165728 | BY165728  |
| 747   | 95   | 3.0 | 459  | 2 | BB633829 | BB633829 | BB633829  |
| 748   | 95   | 3.0 | 519  | 2 | BF046214 | BF046214 | BP250021A |
| 749   | 95   | 3.0 | 541  | 2 | BF045972 | BF045972 | BP250003B |

|   |     |      |     |      |   |          |          |           |
|---|-----|------|-----|------|---|----------|----------|-----------|
|   | 750 | 95   | 3.0 | 542  | 2 | BF039059 | BF039059 | BP250018B |
|   | 751 | 95   | 3.0 | 648  | 6 | CB419189 | CB419189 | 592037 MA |
|   | 752 | 94.8 | 3.0 | 336  | 2 | BB241589 | BB241589 | BB241589  |
|   | 753 | 94.8 | 3.0 | 710  | 6 | CA379066 | CA379066 | 658061 NC |
|   | 754 | 94.8 | 3.0 | 4045 | 3 | BC059007 | BC059007 | Mus muscu |
|   | 755 | 94.6 | 3.0 | 248  | 1 | AV326941 | AV326941 | AV326941  |
|   | 756 | 94.6 | 3.0 | 267  | 2 | BB108706 | BB108706 | BB108706  |
|   | 757 | 94.6 | 3.0 | 278  | 2 | BB479760 | BB479760 | BB479760  |
|   | 758 | 94.6 | 3.0 | 281  | 2 | BB221528 | BB221528 | BB221528  |
|   | 759 | 94.6 | 3.0 | 531  | 2 | BE235013 | BE235013 | 142239 MA |
|   | 760 | 94.6 | 3.0 | 703  | 5 | BM951868 | BM951868 | UI-M-EH0- |
|   | 761 | 94.4 | 3.0 | 275  | 2 | BB336194 | BB336194 | BB336194  |
|   | 762 | 94.4 | 3.0 | 291  | 1 | AV339535 | AV339535 | AV339535  |
|   | 763 | 94.4 | 3.0 | 336  | 2 | BB497526 | BB497526 | BB497526  |
|   | 764 | 94.4 | 3.0 | 520  | 7 | CN255484 | CN255484 | 170005313 |
|   | 765 | 94.4 | 3.0 | 954  | 4 | BG829919 | BG829919 | 602764325 |
|   | 766 | 94.2 | 3.0 | 211  | 2 | BB591302 | BB591302 | BB591302  |
|   | 767 | 94.2 | 3.0 | 481  | 7 | CK392759 | CK392759 | K0849F03- |
|   | 768 | 94.2 | 3.0 | 690  | 6 | BY734086 | BY734086 | BY734086  |
|   | 769 | 94.2 | 3.0 | 819  | 6 | CD628635 | CD628635 | 56097918H |
| c | 770 | 94.2 | 3.0 | 828  | 5 | BX665346 | BX665346 | BX665346  |
|   | 771 | 94   | 3.0 | 230  | 2 | BB254403 | BB254403 | BB254403  |
|   | 772 | 94   | 3.0 | 301  | 2 | BB335163 | BB335163 | BB335163  |
|   | 773 | 94   | 3.0 | 589  | 4 | BM150494 | BM150494 | TCBAP1D10 |
|   | 774 | 93.8 | 3.0 | 227  | 2 | BB213341 | BB213341 | BB213341  |
|   | 775 | 93.8 | 3.0 | 249  | 2 | BB324195 | BB324195 | BB324195  |
|   | 776 | 93.8 | 3.0 | 575  | 2 | BE245715 | BE245715 | TCBAP1D19 |
|   | 777 | 93.6 | 3.0 | 225  | 2 | BB270419 | BB270419 | BB270419  |
|   | 778 | 93.6 | 3.0 | 229  | 2 | BB217995 | BB217995 | BB217995  |
|   | 779 | 93.6 | 3.0 | 237  | 2 | BB431741 | BB431741 | BB431741  |
|   | 780 | 93.6 | 3.0 | 238  | 2 | BB356581 | BB356581 | BB356581  |
|   | 781 | 93.6 | 3.0 | 239  | 1 | AV238091 | AV238091 | AV238091  |
|   | 782 | 93.6 | 3.0 | 241  | 1 | AV341229 | AV341229 | AV341229  |
|   | 783 | 93.6 | 3.0 | 241  | 2 | BB073528 | BB073528 | BB073528  |
|   | 784 | 93.6 | 3.0 | 254  | 2 | BB258946 | BB258946 | BB258946  |
|   | 785 | 93.6 | 3.0 | 259  | 2 | BB215951 | BB215951 | BB215951  |
|   | 786 | 93.6 | 3.0 | 478  | 2 | BF654570 | BF654570 | 278796 MA |
|   | 787 | 93.4 | 3.0 | 244  | 2 | BB519336 | BB519336 | BB519336  |
|   | 788 | 93.2 | 3.0 | 146  | 4 | BI847990 | BI847990 | 470271 MA |
|   | 789 | 93.2 | 3.0 | 244  | 2 | BB242763 | BB242763 | BB242763  |
|   | 790 | 93.2 | 3.0 | 265  | 1 | AV286945 | AV286945 | AV286945  |
| c | 791 | 93.2 | 3.0 | 515  | 1 | AL928354 | AL928354 | AL928354  |
|   | 792 | 93.2 | 3.0 | 2340 | 9 | AY421319 | AY421319 | Mus muscu |
|   | 793 | 93.2 | 3.0 | 3159 | 3 | AK046502 | AK046502 | Mus muscu |
|   | 794 | 93.2 | 3.0 | 3225 | 9 | AY400493 | AY400493 | Mus muscu |
|   | 795 | 93.2 | 3.0 | 3726 | 3 | AK043386 | AK043386 | Mus muscu |
|   | 796 | 93   | 3.0 | 231  | 2 | BB151727 | BB151727 | BB151727  |
|   | 797 | 93   | 3.0 | 527  | 2 | BF462568 | BF462568 | UI-M-CG0p |
|   | 798 | 93   | 3.0 | 725  | 6 | CB520645 | CB520645 | UI-M-GI0- |
|   | 799 | 92.6 | 2.9 | 198  | 4 | BI021066 | BI021066 | PM3-MT020 |
|   | 800 | 92.6 | 2.9 | 228  | 2 | BB073945 | BB073945 | BB073945  |
|   | 801 | 92.6 | 2.9 | 289  | 2 | BB720615 | BB720615 | BB720615  |
|   | 802 | 92.6 | 2.9 | 377  | 5 | BY165251 | BY165251 | BY165251  |
|   | 803 | 92.6 | 2.9 | 546  | 6 | CA406911 | CA406911 | 1003060 H |
|   | 804 | 92.6 | 2.9 | 2575 | 3 | AK031231 | AK031231 | Mus muscu |
|   | 805 | 92.4 | 2.9 | 274  | 2 | BB177348 | BB177348 | BB177348  |
| c | 806 | 92.4 | 2.9 | 404  | 4 | BM174889 | BM174889 | hippo_08_ |

|       |      |     |     |   |          |          |           |
|-------|------|-----|-----|---|----------|----------|-----------|
| 807   | 92.2 | 2.9 | 587 | 5 | BP214222 | BP214222 | BP214222  |
| 808   | 92.2 | 2.9 | 691 | 5 | BM944530 | BM944530 | UI-M-EH0p |
| 809   | 92   | 2.9 | 239 | 2 | BB356352 | BB356352 | BB356352  |
| 810   | 92   | 2.9 | 274 | 2 | BB551851 | BB551851 | BB551851  |
| 811   | 92   | 2.9 | 343 | 2 | BB224139 | BB224139 | BB224139  |
| 812   | 92   | 2.9 | 492 | 7 | CN333872 | CN333872 | 170005325 |
| 813   | 92   | 2.9 | 518 | 2 | BF714462 | BF714462 | mab01a06. |
| 814   | 92   | 2.9 | 748 | 7 | CN333873 | CN333873 | 170006000 |
| 815   | 91.8 | 2.9 | 593 | 7 | CN255490 | CN255490 | 170006000 |
| 816   | 91.8 | 2.9 | 734 | 7 | CO395136 | CO395136 | AGENCOURT |
| 817   | 91.8 | 2.9 | 918 | 7 | CF780707 | CF780707 | AGENCOURT |
| 818   | 91.6 | 2.9 | 247 | 2 | BB170802 | BB170802 | BB170802  |
| c 819 | 91.6 | 2.9 | 434 | 1 | AV608925 | AV608925 | AV608925  |
| 820   | 91.6 | 2.9 | 704 | 6 | CB527136 | CB527136 | UI-M-FY0- |
| 821   | 91.6 | 2.9 | 937 | 5 | BU518484 | BU518484 | AGENCOURT |
| 822   | 91.4 | 2.9 | 433 | 6 | BY580507 | BY580507 | BY580507  |
| 823   | 91.4 | 2.9 | 600 | 5 | BU925145 | BU925145 | 7112-63 M |
| 824   | 91.2 | 2.9 | 281 | 6 | CD631369 | CD631369 | 56027863H |
| 825   | 91.2 | 2.9 | 543 | 6 | CD216128 | CD216128 | pgp2n.pk0 |
| 826   | 91.2 | 2.9 | 756 | 4 | BI645497 | BI645497 | 603275463 |
| 827   | 91   | 2.9 | 229 | 1 | AV232333 | AV232333 | AV232333  |
| 828   | 91   | 2.9 | 625 | 6 | CB247662 | CB247662 | UI-M-FI0- |
| 829   | 91   | 2.9 | 740 | 7 | CF532104 | CF532104 | UI-M-FY0- |
| c 830 | 90.8 | 2.9 | 228 | 6 | CB168395 | CB168395 | HSF603268 |
| 831   | 90.8 | 2.9 | 657 | 7 | CN788571 | CN788571 | 4122921 B |
| 832   | 90.6 | 2.9 | 283 | 1 | AV224722 | AV224722 | AV224722  |
| 833   | 90.6 | 2.9 | 827 | 4 | BF981141 | BF981141 | 602310407 |
| 834   | 90.4 | 2.9 | 230 | 2 | BB270171 | BB270171 | BB270171  |
| 835   | 90.4 | 2.9 | 239 | 2 | BB267673 | BB267673 | BB267673  |
| 836   | 90.4 | 2.9 | 369 | 5 | BY170960 | BY170960 | BY170960  |
| 837   | 90.2 | 2.9 | 238 | 2 | BB356191 | BB356191 | BB356191  |
| 838   | 89.8 | 2.9 | 235 | 2 | BB170781 | BB170781 | BB170781  |
| 839   | 89.8 | 2.9 | 245 | 2 | BB149370 | BB149370 | BB149370  |
| 840   | 89.8 | 2.9 | 896 | 4 | BI457032 | BI457032 | 603185949 |
| 841   | 89.6 | 2.9 | 279 | 2 | BB177200 | BB177200 | BB177200  |
| 842   | 89.4 | 2.8 | 256 | 7 | CN223998 | CN223998 | WLA052F08 |
| 843   | 89.4 | 2.8 | 574 | 5 | BM946983 | BM946983 | UI-M-EH0p |
| 844   | 89.2 | 2.8 | 329 | 2 | BB499916 | BB499916 | BB499916  |
| 845   | 89   | 2.8 | 231 | 2 | BB148551 | BB148551 | BB148551  |
| 846   | 89   | 2.8 | 255 | 2 | BB001987 | BB001987 | BB001987  |
| 847   | 89   | 2.8 | 456 | 5 | BY491040 | BY491040 | BY491040  |
| 848   | 89   | 2.8 | 509 | 2 | AW964929 | AW964929 | EST376897 |
| 849   | 88.8 | 2.8 | 228 | 2 | BB341090 | BB341090 | BB341090  |
| 850   | 88.8 | 2.8 | 232 | 2 | BB009287 | BB009287 | BB009287  |
| 851   | 88.6 | 2.8 | 593 | 5 | BP249762 | BP249762 | BP249762  |
| c 852 | 88.6 | 2.8 | 873 | 5 | BX770216 | BX770216 | BX770216  |
| 853   | 88.2 | 2.8 | 567 | 4 | BG710581 | BG710581 | pg11n.pk0 |
| 854   | 88   | 2.8 | 282 | 2 | BB531669 | BB531669 | BB531669  |
| 855   | 88   | 2.8 | 745 | 6 | CA388534 | CA388534 | 670926 NC |
| 856   | 87.8 | 2.8 | 256 | 5 | BM948107 | BM948107 | UI-M-EG0p |
| 857   | 87.8 | 2.8 | 824 | 4 | BI161136 | BI161136 | 602865179 |
| 858   | 87.4 | 2.8 | 229 | 2 | BB173708 | BB173708 | BB173708  |
| 859   | 87.4 | 2.8 | 234 | 2 | BB717863 | BB717863 | BB717863  |
| 860   | 87.4 | 2.8 | 340 | 5 | BY207534 | BY207534 | BY207534  |
| 861   | 87.4 | 2.8 | 745 | 5 | BU055918 | BU055918 | UI-M-FO0- |
| 862   | 87.2 | 2.8 | 229 | 2 | BB239543 | BB239543 | BB239543  |
| 863   | 87.2 | 2.8 | 240 | 2 | BB326658 | BB326658 | BB326658  |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 864   | 87   | 2.8 | 697  | 2 | AW134401 | AW134401 | fi18h09.y |
| 865   | 87   | 2.8 | 770  | 6 | CD628629 | CD628629 | 56097478H |
| 866   | 86.8 | 2.8 | 242  | 2 | BB359459 | BB359459 | BB359459  |
| 867   | 86.8 | 2.8 | 258  | 1 | AV375018 | AV375018 | AV375018  |
| 868   | 86.6 | 2.8 | 433  | 5 | BY376940 | BY376940 | BY376940  |
| 869   | 86.6 | 2.8 | 917  | 2 | BE908445 | BE908445 | 601503077 |
| 870   | 86.6 | 2.8 | 923  | 4 | BI665624 | BI665624 | 603289613 |
| 871   | 86.6 | 2.8 | 2376 | 3 | AK045236 | AK045236 | Mus muscu |
| 872   | 86.4 | 2.7 | 216  | 2 | BB323957 | BB323957 | BB323957  |
| 873   | 86.4 | 2.7 | 462  | 6 | CD553207 | CD553207 | B0356E10- |
| 874   | 86.4 | 2.7 | 621  | 4 | BM738310 | BM738310 | K-EST0003 |
| 875   | 86.4 | 2.7 | 631  | 6 | BY724321 | BY724321 | BY724321  |
| 876   | 86.4 | 2.7 | 632  | 2 | BE270240 | BE270240 | 601186027 |
| c 877 | 86.4 | 2.7 | 646  | 2 | BF322402 | BF322402 | maa24f04. |
| 878   | 86.4 | 2.7 | 966  | 5 | BQ715428 | BQ715428 | AGENCOURT |
| 879   | 86.2 | 2.7 | 208  | 2 | BB079119 | BB079119 | BB079119  |
| 880   | 86.2 | 2.7 | 242  | 1 | AV381879 | AV381879 | AV381879  |
| 881   | 86.2 | 2.7 | 249  | 2 | BB215799 | BB215799 | BB215799  |
| 882   | 86.2 | 2.7 | 929  | 5 | BQ917819 | BQ917819 | AGENCOURT |
| 883   | 86   | 2.7 | 211  | 2 | BB184958 | BB184958 | BB184958  |
| 884   | 86   | 2.7 | 280  | 2 | BB142942 | BB142942 | BB142942  |
| 885   | 86   | 2.7 | 570  | 2 | BE407695 | BE407695 | 601299714 |
| 886   | 85.8 | 2.7 | 543  | 2 | AW966670 | AW966670 | EST378744 |
| 887   | 85.8 | 2.7 | 757  | 4 | BI735927 | BI735927 | 603360340 |
| 888   | 85.6 | 2.7 | 224  | 2 | BB171694 | BB171694 | BB171694  |
| 889   | 85.6 | 2.7 | 245  | 1 | AV232593 | AV232593 | AV232593  |
| 890   | 85.6 | 2.7 | 673  | 7 | CN401143 | CN401143 | 170005322 |
| 891   | 85.6 | 2.7 | 900  | 6 | CA321459 | CA321459 | UI-M-FW0- |
| 892   | 85.6 | 2.7 | 965  | 5 | BU845252 | BU845252 | AGENCOURT |
| 893   | 85.6 | 2.7 | 977  | 5 | BU855862 | BU855862 | AGENCOURT |
| 894   | 85.4 | 2.7 | 284  | 2 | BB181557 | BB181557 | BB181557  |
| 895   | 85.4 | 2.7 | 356  | 5 | BY204763 | BY204763 | BY204763  |
| 896   | 85.4 | 2.7 | 515  | 2 | BB633428 | BB633428 | BB633428  |
| 897   | 85.2 | 2.7 | 207  | 2 | BB214019 | BB214019 | BB214019  |
| 898   | 85.2 | 2.7 | 620  | 5 | BM943707 | BM943707 | UI-M-EH0p |
| 899   | 85   | 2.7 | 306  | 2 | BB030476 | BB030476 | BB030476  |
| 900   | 84.6 | 2.7 | 232  | 2 | BB262137 | BB262137 | BB262137  |
| 901   | 84.6 | 2.7 | 264  | 2 | BB534094 | BB534094 | BB534094  |
| 902   | 84.6 | 2.7 | 266  | 2 | BB196113 | BB196113 | BB196113  |
| 903   | 84.6 | 2.7 | 698  | 5 | BU227771 | BU227771 | 603800481 |
| 904   | 84.4 | 2.7 | 628  | 6 | CA318117 | CA318117 | UI-M-FW0- |
| 905   | 84.4 | 2.7 | 1010 | 5 | BX360753 | BX360753 | BX360753  |
| 906   | 84.4 | 2.7 | 1246 | 2 | BF166143 | BF166143 | 601776590 |
| 907   | 84.2 | 2.7 | 218  | 2 | BB213301 | BB213301 | BB213301  |
| 908   | 84   | 2.7 | 456  | 5 | BY155480 | BY155480 | BY155480  |
| 909   | 84   | 2.7 | 790  | 6 | CB248961 | CB248961 | UI-M-EX0- |
| 910   | 84   | 2.7 | 864  | 5 | BU156223 | BU156223 | AGENCOURT |
| 911   | 83.8 | 2.7 | 214  | 2 | BB588963 | BB588963 | BB588963  |
| 912   | 83.6 | 2.7 | 249  | 1 | AV381817 | AV381817 | AV381817  |
| 913   | 83.4 | 2.7 | 270  | 2 | BB177951 | BB177951 | BB177951  |
| 914   | 83.4 | 2.7 | 720  | 6 | CD628637 | CD628637 | 56098002H |
| 915   | 83.4 | 2.7 | 777  | 6 | CB248692 | CB248692 | UI-M-EX0- |
| 916   | 83   | 2.6 | 227  | 2 | BB216867 | BB216867 | BB216867  |
| c 917 | 83   | 2.6 | 338  | 6 | CB060198 | CB060198 | 4010590 B |
| 918   | 83   | 2.6 | 691  | 5 | BQ180084 | BQ180084 | UI-M-EW0- |
| 919   | 82.8 | 2.6 | 334  | 5 | BY023564 | BY023564 | BY023564  |
| 920   | 82.8 | 2.6 | 425  | 1 | AV665430 | AV665430 | AV665430  |

|   |     |      |     |      |   |          |          |           |     |
|---|-----|------|-----|------|---|----------|----------|-----------|-----|
|   | 921 | 82.8 | 2.6 | 511  | 6 | CA383610 | CA383610 | 663812    | NC  |
|   | 922 | 82.8 | 2.6 | 647  | 5 | BM950623 | BM950623 | UI-M-EH0p |     |
|   | 923 | 82.6 | 2.6 | 410  | 5 | BU428839 | BU428839 | UI-HF-BN0 |     |
|   | 924 | 82.6 | 2.6 | 445  | 2 | BE244550 | BE244550 | TCBAP1D11 |     |
|   | 925 | 82.6 | 2.6 | 492  | 2 | BE018639 | BE018639 | bb83a12.y |     |
|   | 926 | 82.6 | 2.6 | 549  | 2 | AW655369 | AW655369 | 106098    | MA  |
|   | 927 | 82.6 | 2.6 | 638  | 2 | AW245910 | AW245910 | 2822888.5 |     |
| c | 928 | 82.4 | 2.6 | 139  | 7 | CK942460 | CK942460 | 4066200   | B   |
|   | 929 | 82.4 | 2.6 | 227  | 2 | BB221591 | BB221591 | BB221591  |     |
|   | 930 | 82.4 | 2.6 | 569  | 2 | AW499893 | AW499893 | UI-HF-BN0 |     |
|   | 931 | 82.4 | 2.6 | 582  | 5 | BP348794 | BP348794 | BP348794  |     |
|   | 932 | 82   | 2.6 | 200  | 6 | BY589580 | BY589580 | BY589580  |     |
|   | 933 | 82   | 2.6 | 224  | 2 | BB170950 | BB170950 | BB170950  |     |
|   | 934 | 82   | 2.6 | 314  | 5 | BY347200 | BY347200 | BY347200  |     |
|   | 935 | 82   | 2.6 | 855  | 5 | BQ770087 | BQ770087 | UI-M-FI0- |     |
|   | 936 | 81.8 | 2.6 | 228  | 1 | AV231620 | AV231620 | AV231620  |     |
| c | 937 | 81.6 | 2.6 | 377  | 2 | BE246473 | BE246473 | TCBAP1E47 |     |
|   | 938 | 81.4 | 2.6 | 2292 | 9 | AY402638 | AY402638 | Mus muscu |     |
|   | 939 | 81.2 | 2.6 | 707  | 6 | BY733150 | BY733150 | BY733150  |     |
|   | 940 | 81.2 | 2.6 | 821  | 7 | CK846765 | CK846765 | 969310    | MA  |
|   | 941 | 81   | 2.6 | 553  | 7 | CN684594 | CN684594 | E0195H06- |     |
|   | 942 | 80.8 | 2.6 | 378  | 2 | BB745658 | BB745658 | BB745658  |     |
|   | 943 | 80.8 | 2.6 | 459  | 4 | BJ043336 | BJ043336 | BJ043336  |     |
|   | 944 | 80.8 | 2.6 | 479  | 2 | BF731124 | BF731124 | mab81e06. |     |
|   | 945 | 80.4 | 2.6 | 240  | 2 | BB301102 | BB301102 | BB301102  |     |
|   | 946 | 80.4 | 2.6 | 405  | 6 | CB808856 | CB808856 | AMGNNUC:S |     |
|   | 947 | 80.4 | 2.6 | 625  | 6 | CD348364 | CD348364 | UI-M-FY0- |     |
| c | 948 | 80.4 | 2.6 | 763  | 6 | CD619057 | CD619057 | 56030577H |     |
|   | 949 | 80.4 | 2.6 | 785  | 4 | BI194687 | BI194687 | 602946246 |     |
|   | 950 | 80.4 | 2.6 | 797  | 7 | CO404183 | CO404183 | AGENCOURT |     |
|   | 951 | 80.4 | 2.6 | 890  | 5 | BU856543 | BU856543 | AGENCOURT |     |
|   | 952 | 80.2 | 2.6 | 363  | 5 | BY344602 | BY344602 | BY344602  |     |
|   | 953 | 80.2 | 2.6 | 850  | 5 | BM944264 | BM944264 | UI-M-EH0p |     |
|   | 954 | 80.2 | 2.6 | 900  | 7 | CK799299 | CK799299 | AGENCOURT |     |
| c | 955 | 79.8 | 2.5 | 307  | 4 | BF961259 | BF961259 | PM1-NN120 |     |
|   | 956 | 79.8 | 2.5 | 700  | 6 | CD628633 | CD628633 | 56097902H |     |
|   | 957 | 79.6 | 2.5 | 233  | 2 | BB134411 | BB134411 | BB134411  |     |
|   | 958 | 79.6 | 2.5 | 237  | 2 | BB593564 | BB593564 | BB593564  |     |
|   | 959 | 79.6 | 2.5 | 268  | 2 | BB383954 | BB383954 | BB383954  |     |
| c | 960 | 79.6 | 2.5 | 426  | 4 | BF954455 | BF954455 | MR4-NN020 |     |
|   | 961 | 79.6 | 2.5 | 718  | 4 | BG475468 | BG475468 | 602491461 |     |
|   | 962 | 79.6 | 2.5 | 801  | 5 | BX313585 | BX313585 | BX313585  |     |
|   | 963 | 79.6 | 2.5 | 922  | 5 | BQ943695 | BQ943695 | AGENCOURT |     |
|   | 964 | 79.6 | 2.5 | 2349 | 9 | AY421317 | AY421317 | Homo sapi |     |
|   | 965 | 79.4 | 2.5 | 581  | 5 | BX310430 | BX310430 | BX310430  |     |
|   | 966 | 79.4 | 2.5 | 643  | 5 | BX087763 | BX087763 | BX087763  |     |
|   | 967 | 79.2 | 2.5 | 362  | 5 | BY344235 | BY344235 | BY344235  |     |
| c | 968 | 79.2 | 2.5 | 457  | 2 | AW462107 | AW462107 | BP230008A |     |
|   | 969 | 79.2 | 2.5 | 647  | 2 | BE907509 | BE907509 | 601497468 |     |
|   | 970 | 79   | 2.5 | 295  | 2 | BB354856 | BB354856 | BB354856  |     |
|   | 971 | 79   | 2.5 | 453  | 2 | AW500044 | AW500044 | UI-HF-BN0 |     |
|   | 972 | 79   | 2.5 | 593  | 5 | BQ266902 | BQ266902 | NISC_ff15 |     |
|   | 973 | 79   | 2.5 | 978  | 5 | BQ963608 | BQ963608 | AGENCOURT |     |
|   | 974 | 78.8 | 2.5 | 696  | 7 | CK974651 | CK974651 | 4105581   | B   |
|   | 975 | 78.8 | 2.5 | 826  | 6 | CD628641 | CD628641 | 56097486H |     |
|   | 976 | 78.6 | 2.5 | 474  | 2 | AW659439 | AW659439 | 96609     | MAR |
| c | 977 | 78.6 | 2.5 | 599  | 2 | BF357811 | BF357811 | RC2-LT000 |     |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 978   | 78.4 | 2.5 | 450  | 2 | BE653346 | BE653346 | UI-M-AL1- |
| 979   | 78.4 | 2.5 | 490  | 6 | CA531840 | CA531840 | C0325D06- |
| 980   | 78.4 | 2.5 | 645  | 7 | CF170234 | CF170234 | B0824E08- |
| 981   | 78.4 | 2.5 | 696  | 7 | CF168782 | CF168782 | B0804F02- |
| 982   | 78.4 | 2.5 | 719  | 7 | CK636248 | CK636248 | UI-M-HN0- |
| 983   | 78.2 | 2.5 | 225  | 2 | BB443283 | BB443283 | BB443283  |
| 984   | 78.2 | 2.5 | 231  | 2 | BB148230 | BB148230 | BB148230  |
| c 985 | 78.2 | 2.5 | 254  | 6 | CB469624 | CB469624 | sn09_H09. |
| 986   | 78   | 2.5 | 239  | 2 | BB109818 | BB109818 | BB109818  |
| 987   | 77.8 | 2.5 | 219  | 1 | AV369146 | AV369146 | AV369146  |
| c 988 | 77.8 | 2.5 | 551  | 2 | BF516420 | BF516420 | UI-H-BW1- |
| 989   | 77.6 | 2.5 | 175  | 1 | AV375624 | AV375624 | AV375624  |
| 990   | 77.2 | 2.5 | 887  | 5 | BU906435 | BU906435 | AGENCOURT |
| c 991 | 77   | 2.4 | 703  | 5 | BM936326 | BM936326 | UI-M-CG0p |
| 992   | 76.8 | 2.4 | 438  | 7 | CF535009 | CF535009 | UI-M-GH0- |
| 993   | 76.8 | 2.4 | 687  | 4 | BG327618 | BG327618 | 602426612 |
| 994   | 76.6 | 2.4 | 357  | 1 | AI877089 | AI877089 | vz73g04.r |
| 995   | 76.6 | 2.4 | 443  | 4 | BM484413 | BM484413 | 538266 MA |
| 996   | 76.6 | 2.4 | 469  | 7 | CN429211 | CN429211 | 170005327 |
| 997   | 76.6 | 2.4 | 862  | 1 | AU118557 | AU118557 | AU118557  |
| c 998 | 76.4 | 2.4 | 106  | 6 | CD631365 | CD631365 | 56027747H |
| 999   | 76.2 | 2.4 | 234  | 1 | AV250428 | AV250428 | AV250428  |
| 1000  | 76.2 | 2.4 | 904  | 5 | BU145486 | BU145486 | AGENCOURT |
| 1001  | 76.2 | 2.4 | 2224 | 9 | AY421318 | AY421318 | Pan trogl |
| 1002  | 76   | 2.4 | 77   | 6 | CD631368 | CD631368 | 56027839J |
| 1003  | 76   | 2.4 | 223  | 2 | BB330942 | BB330942 | BB330942  |
| 1004  | 76   | 2.4 | 283  | 6 | CD631364 | CD631364 | 56027739J |
| 1005  | 76   | 2.4 | 600  | 4 | BI986000 | BI986000 | 3154-38 M |
| 1006  | 75.8 | 2.4 | 225  | 2 | BB214723 | BB214723 | BB214723  |
| 1007  | 75.8 | 2.4 | 699  | 6 | CD628631 | CD628631 | 56097494H |
| 1008  | 75.2 | 2.4 | 234  | 2 | BB327897 | BB327897 | BB327897  |
| 1009  | 75.2 | 2.4 | 464  | 2 | BE263633 | BE263633 | 601192057 |
| 1010  | 75.2 | 2.4 | 658  | 4 | BG424478 | BG424478 | 602447602 |
| 1011  | 75.2 | 2.4 | 715  | 5 | BX849809 | BX849809 | BX849809  |
| 1012  | 75.2 | 2.4 | 865  | 5 | BX844237 | BX844237 | BX844237  |
| 1013  | 75.2 | 2.4 | 917  | 5 | BQ224963 | BQ224963 | AGENCOURT |
| 1014  | 75   | 2.4 | 158  | 2 | BB244145 | BB244145 | BB244145  |
| 1015  | 75   | 2.4 | 622  | 6 | CA324358 | CA324358 | UI-M-FY0- |
| 1016  | 75   | 2.4 | 1129 | 5 | BQ071719 | BQ071719 | AGENCOURT |
| c1017 | 74.8 | 2.4 | 462  | 4 | BF944916 | BF944916 | CM1-NN019 |
| c1018 | 74.6 | 2.4 | 130  | 2 | BE349795 | BE349795 | hq43b12.x |
| 1019  | 74.6 | 2.4 | 789  | 4 | BI686539 | BI686539 | 603313631 |
| c1020 | 74.4 | 2.4 | 228  | 1 | AI323583 | AI323583 | mp57e06.x |
| 1021  | 74.4 | 2.4 | 467  | 2 | BF443467 | BF443467 | 260957 MA |
| 1022  | 74.4 | 2.4 | 661  | 7 | CN333878 | CN333878 | 170005315 |
| 1023  | 74.4 | 2.4 | 748  | 7 | CF747865 | CF747865 | UI-M-HE0- |
| 1024  | 74.4 | 2.4 | 763  | 7 | CN461035 | CN461035 | UI-M-HB0- |
| 1025  | 74   | 2.4 | 410  | 2 | AW477508 | AW477508 | 12794 MAR |
| 1026  | 74   | 2.4 | 725  | 7 | CN429210 | CN429210 | 170004241 |
| 1027  | 74   | 2.4 | 771  | 7 | CF285178 | CF285178 | AGENCOURT |
| 1028  | 73.8 | 2.3 | 182  | 2 | BB083305 | BB083305 | BB083305  |
| 1029  | 73.8 | 2.3 | 228  | 1 | AV173854 | AV173854 | AV173854  |
| 1030  | 73.8 | 2.3 | 989  | 6 | CA454865 | CA454865 | AGENCOURT |
| 1031  | 73.6 | 2.3 | 414  | 6 | CB801298 | CB801298 | AMGNNUC:M |
| 1032  | 73.4 | 2.3 | 184  | 2 | BB216676 | BB216676 | BB216676  |
| 1033  | 73.4 | 2.3 | 878  | 4 | BM042998 | BM042998 | 603619122 |
| 1034  | 73.4 | 2.3 | 1019 | 1 | AL541401 | AL541401 | AL541401  |

|       |      |     |      |   |          |          |             |
|-------|------|-----|------|---|----------|----------|-------------|
| 1035  | 73.2 | 2.3 | 154  | 1 | AV230195 | AV230195 | AV230195    |
| 1036  | 73.2 | 2.3 | 430  | 6 | CB760771 | CB760771 | AMGNNUC:T   |
| 1037  | 73.2 | 2.3 | 580  | 7 | CN333883 | CN333883 | 170005318   |
| 1038  | 73   | 2.3 | 275  | 2 | BB604391 | BB604391 | BB604391    |
| c1039 | 73   | 2.3 | 526  | 5 | BX267431 | BX267431 | BX267431    |
| c1040 | 73   | 2.3 | 526  | 5 | BX270851 | BX270851 | BX270851    |
| c1041 | 73   | 2.3 | 528  | 5 | BX270850 | BX270850 | BX270850    |
| 1042  | 73   | 2.3 | 716  | 7 | CF747885 | CF747885 | UI-M-HE0-   |
| 1043  | 73   | 2.3 | 851  | 6 | CD653925 | CD653925 | AGENCOURT   |
| c1044 | 73   | 2.3 | 963  | 9 | CC841964 | CC841964 | NDL.130G1   |
| 1045  | 73   | 2.3 | 3225 | 9 | AY400492 | AY400492 | Pan trogl   |
| c1046 | 72.8 | 2.3 | 355  | 6 | CD631361 | CD631361 | 56027755H   |
| 1047  | 72.8 | 2.3 | 569  | 6 | CA352454 | CA352454 | 623718 NC   |
| 1048  | 72.6 | 2.3 | 636  | 5 | BQ109297 | BQ109297 | imageqc_6   |
| c1049 | 72.6 | 2.3 | 820  | 1 | AI800602 | AI800602 | wg12d10.x   |
| 1050  | 72.2 | 2.3 | 488  | 5 | BQ044885 | BQ044885 | UI-M-EH0p   |
| 1051  | 72.2 | 2.3 | 539  | 7 | CO051028 | CO051028 | Le_mx0_22   |
| 1052  | 72.2 | 2.3 | 843  | 7 | CF995086 | CF995086 | AGENCOURT   |
| 1053  | 72.2 | 2.3 | 914  | 6 | CA792253 | CA792253 | AGENCOURT   |
| 1054  | 71.8 | 2.3 | 228  | 2 | BB213582 | BB213582 | BB213582    |
| 1055  | 71.4 | 2.3 | 680  | 6 | BY735266 | BY735266 | BY735266    |
| 1056  | 71.4 | 2.3 | 715  | 6 | CD628625 | CD628625 | 56097386H   |
| 1057  | 71.4 | 2.3 | 3225 | 9 | AY400491 | AY400491 | Homo sapi   |
| 1058  | 71.2 | 2.3 | 381  | 6 | CB809999 | CB809999 | AMGNNUC:N   |
| c1059 | 71.2 | 2.3 | 396  | 2 | BE245837 | BE245837 | TCBAP1E19   |
| 1060  | 71.2 | 2.3 | 436  | 6 | BY536630 | BY536630 | BY536630    |
| 1061  | 71.2 | 2.3 | 1005 | 5 | BU553834 | BU553834 | AGENCOURT   |
| 1062  | 70.8 | 2.3 | 169  | 7 | CK377833 | CK377833 | lai09b12.   |
| 1063  | 70.8 | 2.3 | 188  | 1 | AV230685 | AV230685 | AV230685    |
| 1064  | 70.8 | 2.3 | 277  | 2 | BB529518 | BB529518 | BB529518    |
| 1065  | 70.8 | 2.3 | 805  | 6 | CD656935 | CD656935 | AGENCOURT   |
| 1066  | 70.6 | 2.2 | 767  | 9 | CL640550 | CL640550 | G076F10 G   |
| c1067 | 70.2 | 2.2 | 151  | 6 | CB475278 | CB475278 | jns105_D0   |
| 1068  | 70.2 | 2.2 | 390  | 9 | CL640447 | CL640447 | G074G07 G   |
| c1069 | 70   | 2.2 | 228  | 1 | AI837906 | AI837906 | UI-M-AL0-   |
| 1070  | 70   | 2.2 | 604  | 2 | BE283742 | BE283742 | 601103987   |
| 1071  | 70   | 2.2 | 777  | 7 | CK479930 | CK479930 | AGENCOURT   |
| 1072  | 70   | 2.2 | 1911 | 9 | AY403380 | AY403380 | Homo sapi   |
| 1073  | 69.8 | 2.2 | 163  | 7 | CF424452 | CF424452 | lad30g10.   |
| c1074 | 69.8 | 2.2 | 285  | 2 | BF874390 | BF874390 | QV2-ET010   |
| 1075  | 69.6 | 2.2 | 157  | 2 | BB151796 | BB151796 | BB151796    |
| 1076  | 69.6 | 2.2 | 266  | 7 | Z28925   | Z28925   | HSBC1H081 S |
| 1077  | 69.6 | 2.2 | 765  | 4 | BI823626 | BI823626 | 603038515   |
| 1078  | 69.6 | 2.2 | 832  | 7 | CN534073 | CN534073 | UI-M-HO0-   |
| 1079  | 69.6 | 2.2 | 1154 | 4 | BM462308 | BM462308 | AGENCOURT   |
| 1080  | 69.4 | 2.2 | 701  | 4 | BI194321 | BI194321 | 602947742   |
| 1081  | 69.2 | 2.2 | 343  | 5 | BY173287 | BY173287 | BY173287    |
| 1082  | 69.2 | 2.2 | 555  | 1 | AI641288 | AI641288 | fc13a11.y   |
| 1083  | 69   | 2.2 | 866  | 4 | BG923853 | BG923853 | 602824656   |
| 1084  | 69   | 2.2 | 894  | 4 | BG422248 | BG422248 | 602446883   |
| 1085  | 68.8 | 2.2 | 638  | 6 | CD215884 | CD215884 | pgp2n.pk0   |
| 1086  | 68.8 | 2.2 | 641  | 7 | CN665211 | CN665211 | A0823B11-   |
| 1087  | 68.8 | 2.2 | 728  | 6 | CD628623 | CD628623 | 56097378H   |
| 1088  | 68.6 | 2.2 | 695  | 5 | BQ769222 | BQ769222 | UI-M-FC0-   |
| c1089 | 68.4 | 2.2 | 325  | 2 | BE246184 | BE246184 | TCBAP2E06   |
| 1090  | 68.4 | 2.2 | 518  | 6 | BY593368 | BY593368 | BY593368    |
| 1091  | 68.2 | 2.2 | 439  | 1 | AA263826 | AA263826 | LD07023.5   |



|       |      |     |      |   |          |          |             |
|-------|------|-----|------|---|----------|----------|-------------|
| 1092  | 68   | 2.2 | 786  | 1 | AL584324 | AL584324 | AL584324    |
| 1093  | 67.8 | 2.2 | 243  | 7 | CO187281 | CO187281 | EK027722.   |
| 1094  | 67.8 | 2.2 | 591  | 1 | AL711630 | AL711630 | DKFZp686N   |
| 1095  | 67.8 | 2.2 | 626  | 7 | CF535272 | CF535272 | UI-M-GH0-   |
| 1096  | 67.8 | 2.2 | 689  | 7 | CN460658 | CN460658 | UI-M-HB0-   |
| 1097  | 67.8 | 2.2 | 849  | 7 | CF726328 | CF726328 | UI-M-HB0-   |
| 1098  | 67.6 | 2.2 | 177  | 2 | BB262424 | BB262424 | BB262424    |
| 1099  | 67.6 | 2.2 | 200  | 2 | BB213365 | BB213365 | BB213365    |
| 1100  | 67.6 | 2.2 | 562  | 4 | BM090629 | BM090629 | igl6e01.y   |
| 1101  | 67.6 | 2.2 | 582  | 5 | BP215174 | BP215174 | BP215174    |
| 1102  | 67.6 | 2.2 | 768  | 6 | CD619058 | CD619058 | 56030577J   |
| 1103  | 67.6 | 2.2 | 4847 | 3 | BC083186 | BC083186 | Mus muscu   |
| 1104  | 67.2 | 2.1 | 238  | 2 | BB593587 | BB593587 | BB593587    |
| 1105  | 67.2 | 2.1 | 394  | 6 | CB547006 | CB547006 | AMGNNUC:S   |
| 1106  | 67.2 | 2.1 | 692  | 7 | CN236752 | CN236752 | RJB124H02   |
| 1107  | 67.2 | 2.1 | 3394 | 3 | AK053632 | AK053632 | Mus muscu   |
| 1108  | 67   | 2.1 | 170  | 2 | BB218573 | BB218573 | BB218573    |
| 1109  | 66.8 | 2.1 | 639  | 7 | CV022901 | CV022901 | 340 Full    |
| c1110 | 66.8 | 2.1 | 710  | 1 | AI638881 | AI638881 | tt08d08.x   |
| 1111  | 66.8 | 2.1 | 967  | 5 | BX460723 | BX460723 | BX460723    |
| 1112  | 66.6 | 2.1 | 185  | 2 | BB008412 | BB008412 | BB008412    |
| 1113  | 66.6 | 2.1 | 291  | 6 | CB710224 | CB710224 | AMGNNUC:N   |
| 1114  | 66.6 | 2.1 | 813  | 6 | CA320357 | CA320357 | UI-M-FW0-   |
| 1115  | 66.4 | 2.1 | 656  | 7 | CF728356 | CF728356 | UI-M-HB0-   |
| 1116  | 66.4 | 2.1 | 777  | 7 | CF742166 | CF742166 | UI-M-HB0-   |
| 1117  | 66.4 | 2.1 | 813  | 2 | BE872958 | BE872958 | 601451552   |
| c1118 | 66.2 | 2.1 | 197  | 2 | AW048928 | AW048928 | UI-M-BH1-   |
| 1119  | 66   | 2.1 | 639  | 6 | CD502318 | CD502318 | CDA56-A04   |
| 1120  | 66   | 2.1 | 801  | 7 | CK679212 | CK679212 | ZF101-P00   |
| 1121  | 65.6 | 2.1 | 668  | 7 | CK836913 | CK836913 | 4062174 B   |
| 1122  | 65.6 | 2.1 | 690  | 4 | BG333712 | BG333712 | 602460715   |
| 1123  | 65.4 | 2.1 | 264  | 2 | BB532400 | BB532400 | BB532400    |
| 1124  | 65.4 | 2.1 | 580  | 5 | BP326398 | BP326398 | BP326398    |
| 1125  | 65.2 | 2.1 | 343  | 5 | BY351503 | BY351503 | BY351503    |
| 1126  | 65.2 | 2.1 | 731  | 7 | CN458596 | CN458596 | UI-M-HB0-   |
| 1127  | 65.2 | 2.1 | 834  | 7 | CF740100 | CF740100 | UI-M-HD0-   |
| 1128  | 65.2 | 2.1 | 1372 | 3 | AK039355 | AK039355 | Mus muscu   |
| 1129  | 65   | 2.1 | 497  | 6 | CA319520 | CA319520 | UI-M-FW0-   |
| 1130  | 65   | 2.1 | 701  | 6 | BY736064 | BY736064 | BY736064    |
| 1131  | 64.8 | 2.1 | 278  | 2 | BB523398 | BB523398 | BB523398    |
| 1132  | 64.8 | 2.1 | 597  | 7 | CN255479 | CN255479 | 170005322   |
| 1133  | 64.8 | 2.1 | 771  | 7 | CK791448 | CK791448 | AGENCOURT   |
| 1134  | 64.6 | 2.1 | 320  | 5 | BY346988 | BY346988 | BY346988    |
| 1135  | 64.2 | 2.0 | 346  | 5 | BY018991 | BY018991 | BY018991    |
| 1136  | 64   | 2.0 | 147  | 1 | AV315332 | AV315332 | AV315332    |
| 1137  | 64   | 2.0 | 576  | 7 | CN333867 | CN333867 | 170005318   |
| 1138  | 64   | 2.0 | 725  | 7 | CN457302 | CN457302 | UI-M-HN0-   |
| 1139  | 64   | 2.0 | 757  | 7 | CK635851 | CK635851 | UI-M-HN0-   |
| 1140  | 64   | 2.0 | 942  | 1 | AU078986 | AU078986 | AU078986    |
| 1141  | 64   | 2.0 | 976  | 9 | CNS02YCR | AL219492 | Tetraodon   |
| 1142  | 64   | 2.0 | 1155 | 2 | BF531775 | BF531775 | 602072681   |
| 1143  | 63.8 | 2.0 | 591  | 4 | BJ074142 | BJ074142 | BJ074142    |
| 1144  | 63.8 | 2.0 | 655  | 4 | BJ063284 | BJ063284 | BJ063284    |
| 1145  | 63.8 | 2.0 | 723  | 4 | BI870437 | BI870437 | 603395690   |
| 1146  | 63.8 | 2.0 | 900  | 6 | C82295   | C82295   | C82295 Leuk |
| 1147  | 63.8 | 2.0 | 2319 | 9 | AY402636 | AY402636 | Homo sapi   |
| 1148  | 63.8 | 2.0 | 2960 | 3 | AK043634 | AK043634 | Mus muscu   |

|       |      |     |      |   |          |          |             |
|-------|------|-----|------|---|----------|----------|-------------|
| 1149  | 63.8 | 2.0 | 3154 | 3 | AK033597 | AK033597 | Mus muscu   |
| 1150  | 63.8 | 2.0 | 3287 | 3 | AK048364 | AK048364 | Mus muscu   |
| 1151  | 63.8 | 2.0 | 3292 | 3 | AK037034 | AK037034 | Mus muscu   |
| 1152  | 63.8 | 2.0 | 3436 | 3 | AK014333 | AK014333 | Mus muscu   |
| 1153  | 63.6 | 2.0 | 233  | 2 | BB327844 | BB327844 | BB327844    |
| 1154  | 63.6 | 2.0 | 573  | 6 | CD214656 | CD214656 | pgm2n.pk0   |
| 1155  | 63.6 | 2.0 | 831  | 7 | CO433634 | CO433634 | UI-M-HX0-   |
| 1156  | 63.4 | 2.0 | 571  | 7 | CN401141 | CN401141 | 170006000   |
| 1157  | 63.4 | 2.0 | 676  | 6 | CD803405 | CD803405 | UI-M-GV0-   |
| 1158  | 63.4 | 2.0 | 889  | 1 | AU050267 | AU050267 | AU050267    |
| 1159  | 63.2 | 2.0 | 700  | 4 | BI143486 | BI143486 | 602907665   |
| 1160  | 63   | 2.0 | 232  | 2 | BB169302 | BB169302 | BB169302    |
| 1161  | 63   | 2.0 | 370  | 5 | BY028015 | BY028015 | BY028015    |
| 1162  | 62.8 | 2.0 | 1020 | 6 | CB590629 | CB590629 | AGENCOURT   |
| 1163  | 62.6 | 2.0 | 214  | 2 | BB269367 | BB269367 | BB269367    |
| c1164 | 62.6 | 2.0 | 384  | 2 | AW900477 | AW900477 | CM0-NN100   |
| 1165  | 62.6 | 2.0 | 469  | 7 | CN429155 | CN429155 | 170005318   |
| 1166  | 62.6 | 2.0 | 508  | 6 | CD675182 | CD675182 | fs20a08.y   |
| 1167  | 62.6 | 2.0 | 602  | 5 | BQ749127 | BQ749127 | UI-M-FD0-   |
| 1168  | 62.6 | 2.0 | 939  | 5 | BU915658 | BU915658 | AGENCOURT   |
| 1169  | 62.4 | 2.0 | 150  | 1 | AV237564 | AV237564 | AV237564    |
| 1170  | 62.4 | 2.0 | 555  | 7 | CN670016 | CN670016 | A0887D08-   |
| 1171  | 62.4 | 2.0 | 2289 | 9 | AY402637 | AY402637 | Pan trogl   |
| 1172  | 62.2 | 2.0 | 178  | 2 | BB603730 | BB603730 | BB603730    |
| 1173  | 62.2 | 2.0 | 857  | 4 | BI161471 | BI161471 | 602865054   |
| 1174  | 62   | 2.0 | 857  | 2 | BF580228 | BF580228 | 602099043   |
| 1175  | 62   | 2.0 | 883  | 5 | BU224821 | BU224821 | 603948128   |
| 1176  | 61.8 | 2.0 | 469  | 1 | AU279333 | AU279333 | AU279333    |
| 1177  | 61.8 | 2.0 | 685  | 1 | AL637843 | AL637843 | AL637843    |
| 1178  | 61.8 | 2.0 | 856  | 7 | CO246694 | CO246694 | AGENCOURT   |
| 1179  | 61.6 | 2.0 | 212  | 2 | BB587253 | BB587253 | BB587253    |
| c1180 | 61.6 | 2.0 | 580  | 7 | CO302404 | CO302404 | EK184063.   |
| 1181  | 61.6 | 2.0 | 859  | 5 | BQ571689 | BQ571689 | UI-M-FC0-   |
| 1182  | 61.4 | 2.0 | 155  | 2 | BB222407 | BB222407 | BB222407    |
| c1183 | 61.4 | 2.0 | 1056 | 9 | CNS00JQN | AL076816 | Drosophil   |
| 1184  | 61.2 | 1.9 | 170  | 2 | BB113286 | BB113286 | BB113286    |
| 1185  | 61.2 | 1.9 | 490  | 7 | CN538039 | CN538039 | UI-M-HS0-   |
| 1186  | 61.2 | 1.9 | 1084 | 4 | BG479750 | BG479750 | 602526948   |
| 1187  | 61   | 1.9 | 203  | 1 | AA326134 | AA326134 | EST29247    |
| c1188 | 61   | 1.9 | 398  | 1 | AI787249 | AI787249 | uj58a10.x   |
| 1189  | 61   | 1.9 | 421  | 7 | CN401145 | CN401145 | 170004241   |
| 1190  | 60.8 | 1.9 | 441  | 6 | CA871124 | CA871124 | K0908A03-   |
| 1191  | 60.8 | 1.9 | 1039 | 5 | BX458912 | BX458912 | BX458912    |
| 1192  | 60.8 | 1.9 | 1170 | 2 | BF345508 | BF345508 | 602019266   |
| 1193  | 60.6 | 1.9 | 207  | 7 | CN700205 | CN700205 | E0431G12-   |
| 1194  | 60.6 | 1.9 | 675  | 6 | BY718955 | BY718955 | BY718955    |
| 1195  | 60.6 | 1.9 | 959  | 1 | AL551337 | AL551337 | AL551337    |
| c1196 | 60   | 1.9 | 395  | 4 | BF947978 | BF947978 | CM1-NN019   |
| c1197 | 60   | 1.9 | 587  | 6 | CB585337 | CB585337 | AMGNNUC:U   |
| 1198  | 59.8 | 1.9 | 812  | 6 | CA317902 | CA317902 | UI-M-FW0-   |
| 1199  | 59.6 | 1.9 | 403  | 7 | CF535184 | CF535184 | UI-M-GI0-   |
| 1200  | 59.6 | 1.9 | 765  | 7 | CK366996 | CK366996 | AGENCOURT   |
| 1201  | 59.4 | 1.9 | 546  | 2 | BF194361 | BF194361 | 246370 MA   |
| 1202  | 59.4 | 1.9 | 736  | 5 | BM947302 | BM947302 | UI-M-EH0p   |
| 1203  | 59.2 | 1.9 | 986  | 4 | BI686422 | BI686422 | 603315567   |
| 1204  | 59   | 1.9 | 265  | 7 | M78717   | M78717   | EST00865 Hi |
| c1205 | 59   | 1.9 | 373  | 4 | BG998374 | BG998374 | PM4-HT130   |

|       |      |     |      |   |          |          |            |
|-------|------|-----|------|---|----------|----------|------------|
| 1206  | 59   | 1.9 | 983  | 5 | BQ879085 | BQ879085 | AGENCOURT  |
| 1207  | 59   | 1.9 | 2227 | 9 | AY403445 | AY403445 | Mus muscu  |
| 1208  | 58.8 | 1.9 | 342  | 2 | BE246502 | BE246502 | TCBAP1D47  |
| c1209 | 58.8 | 1.9 | 595  | 5 | BX672477 | BX672477 | BX672477   |
| c1210 | 58.8 | 1.9 | 718  | 7 | CK776486 | CK776486 | 967641 MA  |
| 1211  | 58.8 | 1.9 | 814  | 2 | BF348116 | BF348116 | 602022006  |
| 1212  | 58.8 | 1.9 | 944  | 5 | BQ931286 | BQ931286 | AGENCOURT  |
| 1213  | 58.6 | 1.9 | 338  | 2 | BE246248 | BE246248 | TCBAP2D06  |
| 1214  | 58.6 | 1.9 | 456  | 4 | BG015017 | BG015017 | PM1-GN018  |
| 1215  | 58.6 | 1.9 | 498  | 1 | AA190645 | AA190645 | zq44a06. r |
| 1216  | 58.6 | 1.9 | 628  | 6 | CB577722 | CB577722 | AMGNNUC:N  |
| 1217  | 58.6 | 1.9 | 987  | 2 | BE727277 | BE727277 | 601560955  |
| 1218  | 58.4 | 1.9 | 581  | 5 | BP198298 | BP198298 | BP198298   |
| 1219  | 58.4 | 1.9 | 595  | 1 | AL678465 | AL678465 | AL678465   |
| 1220  | 58.4 | 1.9 | 599  | 1 | AL678560 | AL678560 | AL678560   |
| 1221  | 58.4 | 1.9 | 766  | 4 | BI335382 | BI335382 | 602997946  |
| 1222  | 58.4 | 1.9 | 1109 | 4 | BM547638 | BM547638 | AGENCOURT  |
| 1223  | 58.4 | 1.9 | 1121 | 4 | BM477901 | BM477901 | AGENCOURT  |
| 1224  | 58.2 | 1.9 | 480  | 5 | BY247585 | BY247585 | BY247585   |
| 1225  | 58.2 | 1.9 | 581  | 5 | BP196129 | BP196129 | BP196129   |
| 1226  | 58.2 | 1.9 | 608  | 1 | AI258757 | AI258757 | LP02029. 5 |
| 1227  | 58.2 | 1.9 | 674  | 1 | AU138132 | AU138132 | AU138132   |
| 1228  | 58.2 | 1.9 | 921  | 2 | BF237200 | BF237200 | 602028155  |
| 1229  | 57.8 | 1.8 | 148  | 1 | AV378912 | AV378912 | AV378912   |
| 1230  | 57.8 | 1.8 | 173  | 2 | AW983563 | AW983563 | RC3-HN000  |
| 1231  | 57.8 | 1.8 | 419  | 6 | CB764881 | CB764881 | AMGNNUC:N  |
| 1232  | 57.8 | 1.8 | 634  | 6 | CB548205 | CB548205 | AMGNNUC:C  |
| 1233  | 57.8 | 1.8 | 634  | 6 | CB577061 | CB577061 | AMGNNUC:C  |
| 1234  | 57.8 | 1.8 | 840  | 6 | CB990331 | CB990331 | AGENCOURT  |
| 1235  | 57.6 | 1.8 | 253  | 6 | CA394719 | CA394719 | cs55b06. y |
| 1236  | 57.6 | 1.8 | 554  | 4 | BI683327 | BI683327 | 464671 MA  |
| 1237  | 57.6 | 1.8 | 574  | 4 | BJ068614 | BJ068614 | BJ068614   |
| 1238  | 57.6 | 1.8 | 631  | 6 | CA876860 | CA876860 | K0951D08-  |
| 1239  | 57.6 | 1.8 | 703  | 4 | BJ733929 | BJ733929 | BJ733929   |
| 1240  | 57.6 | 1.8 | 767  | 7 | CO246012 | CO246012 | AGENCOURT  |
| 1241  | 57.6 | 1.8 | 911  | 5 | BQ278955 | BQ278955 | AGENCOURT  |
| 1242  | 57.4 | 1.8 | 463  | 4 | BI515157 | BI515157 | BB160017B  |
| 1243  | 57.4 | 1.8 | 611  | 5 | BX852769 | BX852769 | BX852769   |
| 1244  | 57.4 | 1.8 | 755  | 4 | BG326539 | BG326539 | 602425385  |
| 1245  | 57.4 | 1.8 | 770  | 6 | CA945576 | CA945576 | UI-M-FD0-  |
| c1246 | 57.2 | 1.8 | 573  | 2 | BE070335 | BE070335 | QV4-BT040  |
| 1247  | 57.2 | 1.8 | 690  | 1 | AU134748 | AU134748 | AU134748   |
| 1248  | 57.2 | 1.8 | 698  | 5 | BX344176 | BX344176 | BX344176   |
| 1249  | 57.2 | 1.8 | 811  | 7 | CK482600 | CK482600 | AGENCOURT  |
| 1250  | 57.2 | 1.8 | 990  | 4 | BI652258 | BI652258 | 603299702  |
| 1251  | 57.2 | 1.8 | 1018 | 4 | BI519944 | BI519944 | 603071726  |
| 1252  | 57   | 1.8 | 444  | 6 | BY531725 | BY531725 | BY531725   |
| 1253  | 57   | 1.8 | 533  | 4 | BI499160 | BI499160 | ie27d02. y |
| 1254  | 57   | 1.8 | 815  | 4 | BI689717 | BI689717 | 603316221  |
| 1255  | 57   | 1.8 | 945  | 7 | CF579434 | CF579434 | AGENCOURT  |
| 1256  | 56.8 | 1.8 | 774  | 7 | CN539668 | CN539668 | UI-M-HU0-  |
| 1257  | 56.8 | 1.8 | 884  | 2 | BE728944 | BE728944 | 601562382  |
| 1258  | 56.8 | 1.8 | 917  | 4 | BI913405 | BI913405 | 603179004  |
| 1259  | 56.6 | 1.8 | 148  | 2 | BB225254 | BB225254 | BB225254   |
| 1260  | 56.6 | 1.8 | 618  | 7 | CN429152 | CN429152 | 170006000  |
| 1261  | 56.6 | 1.8 | 624  | 6 | CB527987 | CB527987 | UI-M-FY0-  |
| c1262 | 56.4 | 1.8 | 148  | 2 | AW045210 | AW045210 | UI-M-BH1-  |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 1263  | 56.4 | 1.8 | 561  | 1 | AA929737 | AA929737 | vz05h07.r |
| c1264 | 56.4 | 1.8 | 576  | 2 | BE831264 | BE831264 | PM2-MT004 |
| 1265  | 56.4 | 1.8 | 589  | 7 | CF179045 | CF179045 | 813129 MA |
| 1266  | 56.4 | 1.8 | 907  | 7 | CF583319 | CF583319 | AGENCOURT |
| c1267 | 56.2 | 1.8 | 117  | 2 | BF470020 | BF470020 | UI-M-BH3- |
| 1268  | 56.2 | 1.8 | 222  | 2 | BB548578 | BB548578 | BB548578  |
| 1269  | 56.2 | 1.8 | 794  | 9 | CL640418 | CL640418 | G074D03 G |
| 1270  | 56   | 1.8 | 822  | 5 | BU208115 | BU208115 | 603952728 |
| 1271  | 55.8 | 1.8 | 656  | 6 | CD628627 | CD628627 | 56097394H |
| 1272  | 55.8 | 1.8 | 670  | 1 | AL870127 | AL870127 | AL870127  |
| c1273 | 55.8 | 1.8 | 717  | 7 | CK225357 | CK225357 | 704281487 |
| 1274  | 55.8 | 1.8 | 1051 | 5 | BQ898681 | BQ898681 | AGENCOURT |
| 1275  | 55.6 | 1.8 | 510  | 1 | AA823166 | AA823166 | vw41e06.r |
| 1276  | 55.6 | 1.8 | 596  | 5 | BP872160 | BP872160 | BP872160  |
| 1277  | 55.4 | 1.8 | 307  | 1 | AA354547 | AA354547 | EST62826  |
| 1278  | 55.4 | 1.8 | 391  | 6 | CB775786 | CB775786 | AMGNNUC:N |
| 1279  | 55.4 | 1.8 | 575  | 7 | CN685188 | CN685188 | E0204H04- |
| 1280  | 55.4 | 1.8 | 599  | 5 | BP218578 | BP218578 | BP218578  |
| 1281  | 55.4 | 1.8 | 637  | 1 | AU135310 | AU135310 | AU135310  |
| 1282  | 55.2 | 1.8 | 258  | 1 | AA601686 | AA601686 | no02b07.s |
| c1283 | 55.2 | 1.8 | 428  | 5 | BX683168 | BX683168 | BX683168  |
| 1284  | 55.2 | 1.8 | 647  | 7 | CK338348 | CK338348 | C0629B03- |
| 1285  | 55.2 | 1.8 | 672  | 6 | BY751398 | BY751398 | BY751398  |
| 1286  | 55.2 | 1.8 | 754  | 7 | CN538762 | CN538762 | UI-M-HS0- |
| 1287  | 55.2 | 1.8 | 1066 | 4 | BG542239 | BG542239 | 602571680 |
| 1288  | 55   | 1.7 | 469  | 4 | BG348876 | BG348876 | de74a05.y |
| 1289  | 55   | 1.7 | 546  | 9 | CG594195 | CG594195 | OST252072 |
| 1290  | 54.6 | 1.7 | 683  | 5 | BU269132 | BU269132 | 603506561 |
| 1291  | 54.6 | 1.7 | 938  | 5 | BU150466 | BU150466 | AGENCOURT |
| 1292  | 54.4 | 1.7 | 486  | 2 | BE982860 | BE982860 | UI-M-CG0p |
| 1293  | 54.4 | 1.7 | 711  | 7 | CK694093 | CK694093 | ZF101-P00 |
| 1294  | 54.4 | 1.7 | 745  | 5 | BU345393 | BU345393 | 603523405 |
| c1295 | 54   | 1.7 | 195  | 1 | AI030698 | AI030698 | UI-R-C0-j |
| 1296  | 54   | 1.7 | 573  | 2 | BF550969 | BF550969 | UI-R-C0-j |
| 1297  | 54   | 1.7 | 598  | 6 | CB434784 | CB434784 | 611453 MA |
| 1298  | 54   | 1.7 | 600  | 5 | BU924827 | BU924827 | 7102-54 M |
| 1299  | 54   | 1.7 | 925  | 9 | CNS0091P | AL053013 | Drosophil |
| 1300  | 54   | 1.7 | 1106 | 6 | CD498549 | CD498549 | CDA34-C01 |
| 1301  | 53.8 | 1.7 | 347  | 7 | CN335013 | CN335013 | 170005360 |
| 1302  | 53.8 | 1.7 | 598  | 4 | BI908590 | BI908590 | 603069993 |
| 1303  | 53.8 | 1.7 | 731  | 7 | CR769103 | CR769103 | DKFZp469L |
| 1304  | 53.6 | 1.7 | 651  | 6 | BY722642 | BY722642 | BY722642  |
| 1305  | 53.4 | 1.7 | 1075 | 5 | BM918793 | BM918793 | AGENCOURT |
| c1306 | 53.4 | 1.7 | 1462 | 3 | CR715185 | CR715185 | Tetraodon |
| 1307  | 53.2 | 1.7 | 562  | 7 | CO322494 | CO322494 | EK188241. |
| 1308  | 53.2 | 1.7 | 595  | 1 | AL876266 | AL876266 | AL876266  |
| 1309  | 53.2 | 1.7 | 785  | 7 | CO428820 | CO428820 | UI-M-HX0- |
| 1310  | 53.2 | 1.7 | 987  | 9 | CNS00418 | AL066537 | Drosophil |
| 1311  | 52.8 | 1.7 | 345  | 4 | BG148558 | BG148558 | uu80g02.y |
| 1312  | 52.8 | 1.7 | 488  | 2 | BF773594 | BF773594 | 283122 MA |
| c1313 | 52.8 | 1.7 | 519  | 6 | CB435264 | CB435264 | 615337 MA |
| 1314  | 52.8 | 1.7 | 787  | 4 | BG783400 | BG783400 | SEAUMC003 |
| 1315  | 52.8 | 1.7 | 809  | 5 | BU232264 | BU232264 | 603410226 |
| 1316  | 52.6 | 1.7 | 442  | 7 | CK392174 | CK392174 | K0842D11- |
| c1317 | 52.6 | 1.7 | 493  | 4 | BG009731 | BG009731 | QV1-GN031 |
| 1318  | 52.6 | 1.7 | 564  | 2 | AW659026 | AW659026 | 95939 MAR |
| 1319  | 52.6 | 1.7 | 626  | 1 | AU137591 | AU137591 | AU137591  |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| c1320 | 52.6 | 1.7 | 760  | 5 | BX919359 | BX919359 | BX919359  |
| 1321  | 52.6 | 1.7 | 787  | 5 | BU610933 | BU610933 | UI-M-FC0- |
| 1322  | 52.6 | 1.7 | 817  | 4 | BG342624 | BG342624 | 602374614 |
| 1323  | 52.6 | 1.7 | 870  | 5 | BU612231 | BU612231 | UI-M-EW0- |
| 1324  | 52.6 | 1.7 | 2307 | 9 | AY407762 | AY407762 | Mus muscu |
| 1325  | 52.4 | 1.7 | 428  | 4 | BI882131 | BI882131 | fm85b03.x |
| 1326  | 52.4 | 1.7 | 525  | 2 | BE260428 | BE260428 | 601150894 |
| 1327  | 52.4 | 1.7 | 621  | 4 | BI066930 | BI066930 | pgfln.pk0 |
| 1328  | 52.4 | 1.7 | 688  | 2 | BE385519 | BE385519 | 601278033 |
| 1329  | 52.4 | 1.7 | 699  | 6 | CA327319 | CA327319 | UI-M-FY0- |
| 1330  | 52.4 | 1.7 | 704  | 4 | BG829860 | BG829860 | 602764154 |
| 1331  | 52.4 | 1.7 | 927  | 5 | BU148244 | BU148244 | AGENCOURT |
| 1332  | 52.4 | 1.7 | 938  | 4 | BG830609 | BG830609 | 602767211 |
| 1333  | 52.2 | 1.7 | 387  | 5 | BY093485 | BY093485 | BY093485  |
| 1334  | 52.2 | 1.7 | 740  | 4 | BG831840 | BG831840 | 602765483 |
| 1335  | 52.2 | 1.7 | 938  | 4 | BG422234 | BG422234 | 602446867 |
| 1336  | 52.2 | 1.7 | 962  | 4 | BG324610 | BG324610 | 602422587 |
| 1337  | 52   | 1.7 | 391  | 4 | BJ620346 | BJ620346 | BJ620346  |
| 1338  | 52   | 1.7 | 479  | 4 | BG010829 | BG010829 | IL5-GN024 |
| 1339  | 52   | 1.7 | 814  | 7 | CK476539 | CK476539 | AGENCOURT |
| 1340  | 52   | 1.7 | 2411 | 6 | CB605722 | CB605722 | AMGNNUC:M |
| 1341  | 51.8 | 1.6 | 576  | 4 | BI067451 | BI067451 | pgfln.pk0 |
| 1342  | 51.8 | 1.6 | 687  | 4 | BI916243 | BI916243 | 603178146 |
| 1343  | 51.8 | 1.6 | 751  | 6 | CA317826 | CA317826 | UI-M-FW0- |
| 1344  | 51.6 | 1.6 | 588  | 5 | BP218616 | BP218616 | BP218616  |
| 1345  | 51.6 | 1.6 | 761  | 7 | CO734982 | CO734982 | SlLE04c10 |
| 1346  | 51.6 | 1.6 | 835  | 7 | CO733414 | CO733414 | SlLT02c05 |
| c1347 | 51.4 | 1.6 | 73   | 6 | CD631367 | CD631367 | 56027839H |
| 1348  | 51.4 | 1.6 | 321  | 7 | CO291094 | CO291094 | EK076120. |
| 1349  | 51.4 | 1.6 | 367  | 6 | CD371550 | CD371550 | UI-R-GO0- |
| 1350  | 51.4 | 1.6 | 533  | 5 | BU484169 | BU484169 | 603469842 |
| 1351  | 51.4 | 1.6 | 647  | 4 | BI067436 | BI067436 | pgfln.pk0 |
| 1352  | 51.4 | 1.6 | 743  | 6 | CA326974 | CA326974 | UI-M-FY0- |
| 1353  | 51.4 | 1.6 | 802  | 5 | BU613129 | BU613129 | UI-M-EW0- |
| 1354  | 51.4 | 1.6 | 1929 | 9 | AY403444 | AY403444 | Pan trogl |
| 1355  | 51.2 | 1.6 | 397  | 6 | CB772279 | CB772279 | AMGNNUC:M |
| 1356  | 51.2 | 1.6 | 582  | 5 | BP349308 | BP349308 | BP349308  |
| c1357 | 51.2 | 1.6 | 659  | 1 | AI651838 | AI651838 | wb55h11.x |
| 1358  | 51.2 | 1.6 | 675  | 2 | BF707801 | BF707801 | A379 LE A |
| 1359  | 51.2 | 1.6 | 728  | 1 | AU137554 | AU137554 | AU137554  |
| 1360  | 51.2 | 1.6 | 748  | 1 | AU136052 | AU136052 | AU136052  |
| 1361  | 51.2 | 1.6 | 773  | 5 | BU515916 | BU515916 | AGENCOURT |
| 1362  | 51.2 | 1.6 | 925  | 4 | BG324814 | BG324814 | 602423928 |
| 1363  | 51.2 | 1.6 | 948  | 4 | BG325041 | BG325041 | 602423476 |
| 1364  | 51   | 1.6 | 478  | 7 | CN290121 | CN290121 | 170005319 |
| 1365  | 51   | 1.6 | 563  | 4 | BI791273 | BI791273 | id03h12.y |
| 1366  | 51   | 1.6 | 755  | 1 | AU137539 | AU137539 | AU137539  |
| 1367  | 51   | 1.6 | 774  | 7 | CN537492 | CN537492 | UI-M-HS0- |
| 1368  | 51   | 1.6 | 804  | 7 | CO430718 | CO430718 | UI-M-HX0- |
| 1369  | 51   | 1.6 | 2227 | 9 | AY403443 | AY403443 | Homo sapi |
| 1370  | 51   | 1.6 | 2596 | 3 | AK053115 | AK053115 | Mus muscu |
| 1371  | 50.8 | 1.6 | 650  | 7 | CR429569 | CR429569 | CR429569  |
| 1372  | 50.8 | 1.6 | 671  | 6 | CD295461 | CD295461 | StrPu691. |
| 1373  | 50.8 | 1.6 | 760  | 2 | BF181876 | BF181876 | 601805303 |
| 1374  | 50.4 | 1.6 | 604  | 4 | BI183160 | BI183160 | UNL-P-FN- |
| 1375  | 50.2 | 1.6 | 283  | 7 | CF136469 | CF136469 | UI-HF-BN0 |
| 1376  | 50.2 | 1.6 | 475  | 9 | CL212177 | CL212177 | G033C05 G |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 1377  | 50.2 | 1.6 | 836  | 7 | CK600018 | CK600018 | AGENCOURT |
| 1378  | 50   | 1.6 | 505  | 2 | BE487489 | BE487489 | 176253 BA |
| 1379  | 50   | 1.6 | 701  | 6 | CB245456 | CB245456 | UI-M-FY0- |
| 1380  | 50   | 1.6 | 735  | 1 | AU140116 | AU140116 | AU140116  |
| 1381  | 49.8 | 1.6 | 519  | 4 | BM741971 | BM741971 | K-EST0014 |
| 1382  | 49.8 | 1.6 | 805  | 5 | BX844812 | BX844812 | BX844812  |
| 1383  | 49.6 | 1.6 | 300  | 7 | CN255485 | CN255485 | 170004251 |
| 1384  | 49.6 | 1.6 | 410  | 6 | CB803735 | CB803735 | AMGNNUC:N |
| 1385  | 49.6 | 1.6 | 549  | 6 | CB614718 | CB614718 | AMGNNUC:N |
| 1386  | 49.6 | 1.6 | 580  | 5 | BU432018 | BU432018 | 603836176 |
| 1387  | 49.6 | 1.6 | 612  | 7 | CN951333 | CN951333 | Ha_mx0_46 |
| 1388  | 49.6 | 1.6 | 773  | 4 | BI218305 | BI218305 | 602934473 |
| 1389  | 49.4 | 1.6 | 410  | 6 | CB153520 | CB153520 | K-EST0210 |
| c1390 | 49.4 | 1.6 | 423  | 4 | BI058070 | BI058070 | PM4-GN050 |
| 1391  | 49.4 | 1.6 | 516  | 6 | CD619063 | CD619063 | 56053362H |
| 1392  | 49.4 | 1.6 | 516  | 6 | CD619065 | CD619065 | 56053454H |
| c1393 | 49.4 | 1.6 | 538  | 6 | CD619064 | CD619064 | 56053362J |
| c1394 | 49.4 | 1.6 | 550  | 6 | CD619062 | CD619062 | 56053346J |
| c1395 | 49.4 | 1.6 | 551  | 6 | CD619060 | CD619060 | 56053340J |
| c1396 | 49.4 | 1.6 | 552  | 6 | CD619066 | CD619066 | 56053454J |
| 1397  | 49.4 | 1.6 | 559  | 6 | CA872840 | CA872840 | K0920H08- |
| 1398  | 49.4 | 1.6 | 595  | 5 | BP271999 | BP271999 | BP271999  |
| 1399  | 49.4 | 1.6 | 688  | 4 | BI552143 | BI552143 | 603195086 |
| 1400  | 49.4 | 1.6 | 749  | 9 | CNS02V9F | AL215484 | Tetraodon |
| 1401  | 49.4 | 1.6 | 766  | 4 | BG825242 | BG825242 | 602747664 |
| 1402  | 49.4 | 1.6 | 771  | 4 | BI859915 | BI859915 | 603386049 |
| 1403  | 49.4 | 1.6 | 910  | 9 | CNS033DR | AL226008 | Tetraodon |
| 1404  | 49.2 | 1.6 | 542  | 4 | BM740534 | BM740534 | K-EST0011 |
| 1405  | 49.2 | 1.6 | 544  | 4 | BM766233 | BM766233 | K-EST0048 |
| 1406  | 49.2 | 1.6 | 626  | 4 | BM740685 | BM740685 | K-EST0012 |
| c1407 | 49.2 | 1.6 | 897  | 9 | CG766342 | CG766342 | TcB48.4_B |
| c1408 | 49.2 | 1.6 | 898  | 9 | CG770102 | CG770102 | TcB51.2_A |
| c1409 | 49.2 | 1.6 | 901  | 5 | BQ433090 | BQ433090 | AGENCOURT |
| 1410  | 49.2 | 1.6 | 904  | 5 | BQ735037 | BQ735037 | AGENCOURT |
| 1411  | 49.2 | 1.6 | 1177 | 5 | BM906470 | BM906470 | AGENCOURT |
| 1412  | 49.2 | 1.6 | 1309 | 5 | BU541920 | BU541920 | AGENCOURT |
| c1413 | 49   | 1.6 | 293  | 6 | CD631363 | CD631363 | 56027739H |
| c1414 | 49   | 1.6 | 695  | 7 | CK225361 | CK225361 | 704197850 |
| 1415  | 49   | 1.6 | 1161 | 3 | CR679362 | CR679362 | Tetraodon |
| c1416 | 48.8 | 1.6 | 372  | 1 | AA984436 | AA984436 | am86d04.s |
| 1417  | 48.8 | 1.6 | 412  | 6 | CB801382 | CB801382 | AMGNNUC:M |
| 1418  | 48.8 | 1.6 | 473  | 8 | AQ603447 | AQ603447 | HS_2126_A |
| 1419  | 48.8 | 1.6 | 610  | 2 | BB613257 | BB613257 | BB613257  |
| 1420  | 48.8 | 1.6 | 726  | 7 | CN042616 | CN042616 | v11_p43_g |
| 1421  | 48.6 | 1.5 | 431  | 6 | CB757701 | CB757701 | AMGNNUC:M |
| 1422  | 48.6 | 1.5 | 702  | 4 | BI771035 | BI771035 | 603055382 |
| 1423  | 48.6 | 1.5 | 1809 | 3 | AK051165 | AK051165 | Mus muscu |
| 1424  | 48.6 | 1.5 | 3317 | 3 | AK052671 | AK052671 | Mus muscu |
| 1425  | 48.6 | 1.5 | 3672 | 3 | AK028900 | AK028900 | Mus muscu |
| 1426  | 48.6 | 1.5 | 4248 | 3 | AK031704 | AK031704 | Mus muscu |
| 1427  | 48.4 | 1.5 | 416  | 5 | BY224521 | BY224521 | BY224521  |
| 1428  | 48.4 | 1.5 | 539  | 1 | AL918018 | AL918018 | AL918018  |
| 1429  | 48.2 | 1.5 | 428  | 6 | CB794320 | CB794320 | AMGNNUC:N |
| 1430  | 48.2 | 1.5 | 640  | 6 | CA334086 | CA334086 | NISC_ls05 |
| 1431  | 48.2 | 1.5 | 876  | 6 | CA489866 | CA489866 | AGENCOURT |
| 1432  | 48   | 1.5 | 384  | 6 | CB703233 | CB703233 | AMGNNUC:N |
| 1433  | 48   | 1.5 | 569  | 4 | BI775284 | BI775284 | 467707 MA |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 1434  | 48   | 1.5 | 817  | 7 | CF994909 | CF994909 | AGENCOURT |
| c1435 | 48   | 1.5 | 963  | 5 | BX341410 | BX341410 | BX341410  |
| 1436  | 47.8 | 1.5 | 253  | 4 | BF988853 | BF988853 | IL5-GN017 |
| 1437  | 47.8 | 1.5 | 254  | 4 | BM030705 | BM030705 | 495185 MA |
| 1438  | 47.8 | 1.5 | 406  | 6 | CB808351 | CB808351 | AMGNNUC:S |
| c1439 | 47.8 | 1.5 | 420  | 2 | AW803853 | AW803853 | IL2-UM008 |
| c1440 | 47.8 | 1.5 | 537  | 6 | CB717637 | CB717637 | AMGNNUC:U |
| 1441  | 47.8 | 1.5 | 633  | 7 | CN295126 | CN295126 | 170005326 |
| 1442  | 47.8 | 1.5 | 975  | 2 | BF101157 | BF101157 | 601754732 |
| 1443  | 47.6 | 1.5 | 619  | 4 | BI648895 | BI648895 | 603275856 |
| 1444  | 47.6 | 1.5 | 709  | 6 | CD348531 | CD348531 | UI-M-FY0- |
| 1445  | 47.6 | 1.5 | 777  | 5 | BU708565 | BU708565 | UI-M-FI0- |
| c1446 | 47.6 | 1.5 | 796  | 1 | AL561140 | AL561140 | AL561140  |
| 1447  | 47.6 | 1.5 | 1911 | 9 | AY403382 | AY403382 | Mus muscu |
| c1448 | 47.4 | 1.5 | 240  | 4 | BI000873 | BI000873 | MR3-HN006 |
| c1449 | 47.4 | 1.5 | 469  | 1 | AA859662 | AA859662 | UI-R-E0-b |
| 1450  | 47.4 | 1.5 | 613  | 5 | BX271575 | BX271575 | BX271575  |
| 1451  | 47.2 | 1.5 | 645  | 4 | BI066459 | BI066459 | pgfln.pk0 |
| 1452  | 47.2 | 1.5 | 654  | 2 | BB037994 | BB037994 | BB037994  |
| c1453 | 47.2 | 1.5 | 737  | 9 | CR018931 | CR018931 | Reverse s |
| 1454  | 47.2 | 1.5 | 775  | 5 | BU703431 | BU703431 | UI-M-FO0- |
| 1455  | 47.2 | 1.5 | 1023 | 6 | CD245257 | CD245257 | AGENCOURT |
| c1456 | 47   | 1.5 | 367  | 5 | BQ320183 | BQ320183 | PM4-CT082 |
| 1457  | 47   | 1.5 | 480  | 7 | CR579310 | CR579310 | CR579310  |
| 1458  | 47   | 1.5 | 511  | 4 | BI673056 | BI673056 | ft33e03.y |
| 1459  | 47   | 1.5 | 516  | 6 | CD619061 | CD619061 | 56053346H |
| 1460  | 47   | 1.5 | 543  | 1 | AA940432 | AA940432 | vz48h07.r |
| 1461  | 47   | 1.5 | 625  | 4 | BI753404 | BI753404 | 603026593 |
| 1462  | 47   | 1.5 | 834  | 7 | CF149484 | CF149484 | AGENCOURT |
| 1463  | 46.8 | 1.5 | 350  | 5 | BY200122 | BY200122 | BY200122  |
| 1464  | 46.8 | 1.5 | 365  | 2 | AW437778 | AW437778 | 79230 MAR |
| 1465  | 46.8 | 1.5 | 635  | 1 | AL852575 | AL852575 | AL852575  |
| c1466 | 46.8 | 1.5 | 741  | 2 | BF232471 | BF232471 | de06c04.x |
| 1467  | 46.8 | 1.5 | 932  | 9 | CNS022IX | AL178242 | Tetraodon |
| 1468  | 46.8 | 1.5 | 950  | 5 | BU175283 | BU175283 | AGENCOURT |
| c1469 | 46.8 | 1.5 | 1131 | 5 | BM922197 | BM922197 | AGENCOURT |
| 1470  | 46.6 | 1.5 | 533  | 1 | AA175711 | AA175711 | ms97a05.r |
| 1471  | 46.6 | 1.5 | 609  | 4 | BI066327 | BI066327 | pgfln.pk0 |
| 1472  | 46.6 | 1.5 | 641  | 6 | BY728676 | BY728676 | BY728676  |
| 1473  | 46.6 | 1.5 | 688  | 4 | BG700674 | BG700674 | 602682306 |
| 1474  | 46.4 | 1.5 | 395  | 6 | CB773879 | CB773879 | AMGNNUC:N |
| c1475 | 46.4 | 1.5 | 678  | 9 | CC569313 | CC569313 | CH240_444 |
| 1476  | 46.4 | 1.5 | 957  | 4 | BG261855 | BG261855 | 602373655 |
| 1477  | 46.4 | 1.5 | 971  | 4 | BG342228 | BG342228 | 602374305 |
| c1478 | 46.4 | 1.5 | 985  | 5 | BX402983 | BX402983 | BX402983  |
| 1479  | 46.4 | 1.5 | 994  | 5 | BQ929877 | BQ929877 | AGENCOURT |
| 1480  | 46.2 | 1.5 | 564  | 7 | CK635703 | CK635703 | UI-M-HN0- |
| 1481  | 46.2 | 1.5 | 570  | 2 | BE033028 | BE033028 | 133242 MA |
| 1482  | 46.2 | 1.5 | 590  | 9 | AY420627 | AY420627 | Homo sapi |
| 1483  | 46.2 | 1.5 | 594  | 7 | CN409468 | CN409468 | 170004276 |
| 1484  | 46.2 | 1.5 | 624  | 2 | AW328571 | AW328571 | ds03dl2.x |
| 1485  | 46.2 | 1.5 | 634  | 5 | BM951500 | BM951500 | UI-M-EG0- |
| 1486  | 46.2 | 1.5 | 650  | 7 | CF746951 | CF746951 | UI-M-HE0- |
| 1487  | 46.2 | 1.5 | 658  | 7 | CN409465 | CN409465 | 170005325 |
| 1488  | 46.2 | 1.5 | 678  | 7 | CN409457 | CN409457 | 170004177 |
| 1489  | 46.2 | 1.5 | 732  | 7 | CN409463 | CN409463 | 170005325 |
| 1490  | 46.2 | 1.5 | 732  | 7 | CN531114 | CN531114 | UI-M-HO0- |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 1491  | 46.2 | 1.5 | 741  | 7 | CF730435 | CF730435 | UI-M-GZ0- |
| 1492  | 46.2 | 1.5 | 778  | 7 | CF736303 | CF736303 | UI-M-HD0- |
| 1493  | 46   | 1.5 | 394  | 6 | CB776561 | CB776561 | AMGNNUC:S |
| c1494 | 46   | 1.5 | 428  | 1 | AI458053 | AI458053 | tj66h10.x |
| 1495  | 46   | 1.5 | 528  | 2 | BE334076 | BE334076 | us29e10.y |
| 1496  | 46   | 1.5 | 575  | 5 | BP338720 | BP338720 | BP338720  |
| 1497  | 46   | 1.5 | 714  | 7 | CR789306 | CR789306 | DKFZp4590 |
| 1498  | 46   | 1.5 | 2775 | 3 | AK077021 | AK077021 | Mus muscu |
| 1499  | 45.8 | 1.5 | 372  | 2 | BF443919 | BF443919 | 261588 MA |
| 1500  | 45.8 | 1.5 | 375  | 6 | CB691762 | CB691762 | AMGNNUC:M |

# ALIGNMENTS

## RESULT 1

CR623694

LOCUS CR623694 3005 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CSODL005YC17 of B cells (Ramos cell line)  
Cot 25-normalized of Homo sapiens (human).

ACCESSION CR623694

VERSION CR623694.1 GI:50504501

KEYWORDS HTC; CNSLT\_cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3005)

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600  
Faraday Avenue

REFERENCE 2 (bases 1 to 3005)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES Location/Qualifiers

source

1. .3005

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CSODL005YC17"

/tissue\_type="B cells (Ramos cell line) Cot 25-normalized"

/plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 95.6%; Score 3005; DB 3; Length 3005;

Best Local Similarity 100.0%; Pred. No. 0;



Matches 3005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 99  | CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC | 158 |
|    |     |  |     |
| Db | 1   | CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC | 60  |
| Qy | 159 | TTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCC  | 218 |
|    |     |  |     |
| Db | 61  | TTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCC  | 120 |
| Qy | 219 | ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG | 278 |
|    |     |  |     |
| Db | 121 | ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG | 180 |
| Qy | 279 | AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG | 338 |
|    |     |  |     |
| Db | 181 | AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG | 240 |
| Qy | 339 | GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGTCCCCAGGCTAAAG  | 398 |
|    |     |  |     |
| Db | 241 | GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGTCCCCAGGCTAAAG  | 300 |
| Qy | 399 | AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG | 458 |
|    |     |  |     |
| Db | 301 | AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG | 360 |
| Qy | 459 | AGCAATGAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT  | 518 |
|    |     |  |     |
| Db | 361 | AGCAATGAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT  | 420 |
| Qy | 519 | CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT | 578 |
|    |     |  |     |
| Db | 421 | CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT | 480 |
| Qy | 579 | TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCTTT   | 638 |
|    |     |  |     |
| Db | 481 | TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCTTT   | 540 |
| Qy | 639 | GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG | 698 |
|    |     |  |     |
| Db | 541 | GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG | 600 |
| Qy | 699 | AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC | 758 |
|    |     |  |     |
| Db | 601 | AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC | 660 |
| Qy | 759 | AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT | 818 |
|    |     |  |     |
| Db | 661 | AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT | 720 |
| Qy | 819 | TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG | 878 |
|    |     |  |     |
| Db | 721 | TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG | 780 |
| Qy | 879 | AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG | 938 |
|    |     |  |     |
| Db | 781 | AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG | 840 |

|    |      |  |      |
|----|------|--|------|
| Qy | 939  | CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAG  | 998  |
|    |      |  |      |
| Db | 841  | CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAG  | 900  |
| Qy | 999  | CTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCC  | 1058 |
|    |      |  |      |
| Db | 901  | CTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCC  | 960  |
| Qy | 1059 | CACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTT | 1118 |
|    |      |  |      |
| Db | 961  | CACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTT | 1020 |
| Qy | 1119 | TGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAAC | 1178 |
|    |      |  |      |
| Db | 1021 | TGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAAC | 1080 |
| Qy | 1179 | AAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGCCAGGCAGT  | 1238 |
|    |      |  |      |
| Db | 1081 | AAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGCCAGGCAGT  | 1140 |
| Qy | 1239 | TGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATG | 1298 |
|    |      |  |      |
| Db | 1141 | TGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATG | 1200 |
| Qy | 1299 | GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT | 1358 |
|    |      |  |      |
| Db | 1201 | GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT | 1260 |
| Qy | 1359 | GCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC | 1418 |
|    |      |  |      |
| Db | 1261 | GCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC | 1320 |
| Qy | 1419 | ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA | 1478 |
|    |      |  |      |
| Db | 1321 | ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA | 1380 |
| Qy | 1479 | GAGATTGAGCTGTTCCCTGACCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAG    | 1538 |
|    |      |  |      |
| Db | 1381 | GAGATTGAGCTGTTCCCTGACCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAG    | 1440 |
| Qy | 1539 | GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT | 1598 |
|    |      |  |      |
| Db | 1441 | GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT | 1500 |
| Qy | 1599 | GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT | 1658 |
|    |      |  |      |
| Db | 1501 | GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT | 1560 |
| Qy | 1659 | GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCTGGAAGCAGGACATG  | 1718 |
|    |      |  |      |
| Db | 1561 | GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCTGGAAGCAGGACATG  | 1620 |
| Qy | 1719 | GAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT | 1778 |
|    |      |  |      |
| Db | 1621 | GAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT | 1680 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1779 | CAGAGCCGCCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC  | 1838 |
|    |      |   |      |
| Db | 1681 | CAGAGCCGCCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC  | 1740 |
| Qy | 1839 | CCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC   | 1898 |
|    |      |   |      |
| Db | 1741 | CCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC   | 1800 |
| Qy | 1899 | CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT  | 1958 |
|    |      |   |      |
| Db | 1801 | CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT  | 1860 |
| Qy | 1959 | GGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC  | 2018 |
|    |      |   |      |
| Db | 1861 | GGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC  | 1920 |
| Qy | 2019 | TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGG   | 2078 |
|    |      |   |      |
| Db | 1921 | TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGG   | 1980 |
| Qy | 2079 | GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG  | 2138 |
|    |      |   |      |
| Db | 1981 | GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG  | 2040 |
| Qy | 2139 | TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCC  | 2198 |
|    |      |   |      |
| Db | 2041 | TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCC  | 2100 |
| Qy | 2199 | CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGC | 2258 |
|    |      |   |      |
| Db | 2101 | CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGC | 2160 |
| Qy | 2259 | TGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCT  | 2318 |
|    |      |   |      |
| Db | 2161 | TGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCT  | 2220 |
| Qy | 2319 | CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACT | 2378 |
|    |      |   |      |
| Db | 2221 | CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACT | 2280 |
| Qy | 2379 | GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG  | 2438 |
|    |      |   |      |
| Db | 2281 | GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG  | 2340 |
| Qy | 2439 | CTGGGCGGCCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC | 2498 |
|    |      |   |      |
| Db | 2341 | CTGGGCGGCCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC | 2400 |
| Qy | 2499 | CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG  | 2558 |
|    |      |   |      |
| Db | 2401 | CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG  | 2460 |
| Qy | 2559 | CAGTCTGCCTCCCCATATGGGACTCCCTTCTACCAAGCACATGAGCTCTTAACAGGGTGG  | 2618 |
|    |      |   |      |
| Db | 2461 | CAGTCTGCCTCCCCATATGGGACTCCCTTCTACCAAGCACATGAGCTCTTAACAGGGTGG  | 2520 |
| Qy | 2619 | GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT  | 2678 |

|    |      |   |      |
|----|------|---|------|
| Db | 2521 | GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT  | 2580 |
| Qy | 2679 | TCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGC  | 2738 |
| Db | 2581 | TCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGC  | 2640 |
| Qy | 2739 | CTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGC  | 2798 |
| Db | 2641 | CTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGC  | 2700 |
| Qy | 2799 | CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCAG   | 2858 |
| Db | 2701 | CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCAG   | 2760 |
| Qy | 2859 | GGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCA  | 2918 |
| Db | 2761 | GGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCA  | 2820 |
| Qy | 2919 | GGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGGCAGACTCTGAT   | 2978 |
| Db | 2821 | GGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGGCAGACTCTGAT   | 2880 |
| Qy | 2979 | CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG  | 3038 |
| Db | 2881 | CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG  | 2940 |
| Qy | 3039 | CTGACCCCTTCACCTCTCCCCCTCCCTTTTCTTTGTTTTGGGATTTCAGAAAACCTGCTTG | 3098 |
| Db | 2941 | CTGACCCCTTCACCTCTCCCCCTCCCTTTTCTTTGTTTTGGGATTTCAGAAAACCTGCTTG | 3000 |
| Qy | 3099 | TCAGA 3103  |      |
| Db | 3001 | TCAGA 3005  |      |

RESULT 2  
HSM807023

|            |   |         |      |        |                 |
|------------|---|---------|------|--------|-----------------|
| LOCUS      | HSM807023   | 3151 bp | mRNA | linear | HTC 22-SEP-2004 |
| DEFINITION | Homo sapiens mRNA; cDNA DKFZp686D04248 (from clone DKFZp686D04248).   |         |      |        |                 |
| ACCESSION  | BX640891  |         |      |        |                 |
| VERSION    | BX640891.1 GI:34365195  |         |      |        |                 |
| KEYWORDS   | HTC.  |         |      |        |                 |
| SOURCE     | Homo sapiens (human)  |         |      |        |                 |
| ORGANISM   | Homo sapiens  |         |      |        |                 |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.          |         |      |        |                 |
| REFERENCE  | 1 (bases 1 to 3151)   |         |      |        |                 |
| AUTHORS    | Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S. |         |      |        |                 |
| CONSRM     | The German cDNA Consortium  |         |      |        |                 |
| TITLE      | Direct Submission   |         |      |        |                 |
| JOURNAL    | Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY  |         |      |        |                 |
| COMMENT    | Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;           |         |      |        |                 |

sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686D04248) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:  
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686D04248>  
 Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

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FEATURES
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#### ORIGIN

Query Match 93.1%; Score 2927.6; DB 3; Length 3151;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2933; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy      202 GAGGCGGGCAGGGGCCCATGCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCAC 261
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| Qy | 322  | GAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAG  | 381  |
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| Qy | 382  | GGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAAT  | 441  |
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| Db | 380  | GGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAAT  | 439  |
| Qy | 442  | GTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGT    | 501  |
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| Db | 440  | GTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGT    | 499  |
| Qy | 502  | CTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCT | 561  |
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| Db | 500  | CTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCT | 559  |
| Qy | 562  | TCATTGAACTTCAAGATTCCCTACCTGTTGCCATCTCGGAGGACAAGGTCATGGAGGGAA  | 621  |
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| Db | 560  | TCATTGAACTTCAAGATTCCCTACCTGTTGCCATCTCGGAGGACAAGGTCATGGAGGGAA  | 619  |
| Qy | 622  | AAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGC  | 681  |
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| Db | 620  | AAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGC  | 679  |
| Qy | 682  | TCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGG  | 741  |
|    |      |   |      |
| Db | 680  | TCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGG  | 739  |
| Qy | 742  | GATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCT  | 801  |
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| Db | 740  | GATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCT  | 799  |
| Qy | 802  | TTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCG  | 861  |
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| Db | 800  | TTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCG  | 859  |
| Qy | 862  | AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG  | 921  |
|    |      |   |      |
| Db | 860  | AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG  | 919  |
| Qy | 922  | TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCT   | 981  |
|    |      |   |      |
| Db | 920  | TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCT   | 979  |
| Qy | 982  | GCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCG    | 1041 |
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| Db | 980  | GCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCG    | 1039 |
| Qy | 1042 | ATTCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGA    | 1101 |
|    |      |   |      |
| Db | 1040 | ATTCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGA    | 1099 |
| Qy | 1102 | CCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGA  | 1161 |
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| Db | 1100 | CCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGA  | 1159 |
| Qy | 1162 | AATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCA   | 1221 |

|    |      |  |      |
|----|------|--|------|
| Db | 1160 | <br>AATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGGCCCTGAGACCA  | 1219 |
| Qy | 1222 | <br>ACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGA  | 1281 |
| Db | 1220 | <br>ACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGA  | 1279 |
| Qy | 1282 | <br>AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCG   | 1341 |
| Db | 1280 | <br>AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCG   | 1339 |
| Qy | 1342 | <br>TGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTG   | 1401 |
| Db | 1340 | <br>TGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTG   | 1399 |
| Qy | 1402 | <br>TCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCA   | 1461 |
| Db | 1400 | <br>TCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCA   | 1459 |
| Qy | 1462 | <br>GTGCTCATCTGGTGGGAAGAGATTGAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGC | 1521 |
| Db | 1460 | <br>GTGCTCATCTGGTGGGAAGAGATTGAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGC | 1519 |
| Qy | 1522 | <br>AGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCCTGGAGGGTGC   | 1581 |
| Db | 1520 | <br>AGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCCTGGAGGGTGC   | 1579 |
| Qy | 1582 | <br>CCCAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCCGGGACCCCC    | 1641 |
| Db | 1580 | <br>CCCAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCCGGGACCCCC    | 1639 |
| Qy | 1642 | <br>ACTGTGCCTGGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACT     | 1701 |
| Db | 1640 | <br>ACTGTGCCTGGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACT     | 1699 |
| Qy | 1702 | <br>CCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGA   | 1761 |
| Db | 1700 | <br>CCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGA   | 1759 |
| Qy | 1762 | <br>GCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCA    | 1821 |
| Db | 1760 | <br>GCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCA    | 1819 |
| Qy | 1822 | <br>ACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGCCCTCTTATTATTGGAGTC    | 1881 |
| Db | 1820 | <br>ACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGCCCTCTTATTATTGGAGTC    | 1879 |
| Qy | 1882 | <br>ATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGA   | 1941 |
| Db | 1880 | <br>ATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGA   | 1939 |
| Qy | 1942 | <br>TAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGTGGGCAACTGAGAATGGCTTTTCAT    | 2001 |
| Db | 1940 | <br>TAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGTGGGCAACTGAGAATGGCTTTTCAT    | 1999 |
| Qy | 2002 | <br>ACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAC   | 2061 |

|    |      |  |      |
|----|------|--|------|
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| Qy | 2062 | TGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG    | 2121 |
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| Db | 2060 | TGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG    | 2119 |
| Qy | 2122 | CCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACGTGTCACGTGTCCTCTTTGCCT | 2181 |
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| Db | 2120 | CCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACGTGTCACGTGTCCTCTTTGCCT | 2179 |
| Qy | 2182 | TAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTC  | 2241 |
|    |      |  |      |
| Db | 2180 | TAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTC  | 2239 |
| Qy | 2242 | GGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAG  | 2301 |
|    |      |  |      |
| Db | 2240 | GGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAG  | 2299 |
| Qy | 2302 | AGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACA   | 2361 |
|    |      |  |      |
| Db | 2300 | AGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACA   | 2359 |
| Qy | 2362 | ACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAG   | 2421 |
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| Db | 2360 | ACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAG   | 2419 |
| Qy | 2422 | GCACCTGGCCATGCTGGCTGGGCGGCCCCAAGCACAGCCCTGACTAGGATGACAGCAGCAC  | 2481 |
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| Db | 2420 | GCACCTGGCCATGCTGGCTGGGCGGCCCCAAGCACAGCCCTGACTAGGATGACAGCAGCAC  | 2479 |
| Qy | 2482 | AAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTC   | 2541 |
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| Db | 2480 | AAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTC   | 2539 |
| Qy | 2542 | AGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGA   | 2601 |
|    |      |  |      |
| Db | 2540 | AGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGA   | 2599 |
| Qy | 2602 | GCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCT   | 2661 |
|    |      |  |      |
| Db | 2600 | GCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCT   | 2659 |
| Qy | 2662 | GGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGA   | 2721 |
|    |      |  |      |
| Db | 2660 | GGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGA   | 2719 |
| Qy | 2722 | GACCCATAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACA  | 2781 |
|    |      |  |      |
| Db | 2720 | GACCCATAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACA  | 2779 |
| Qy | 2782 | ATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCA   | 2841 |
|    |      |  |      |
| Db | 2780 | ATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCA   | 2839 |
| Qy | 2842 | ACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCG   | 2901 |
|    |      |  |      |
| Db | 2840 | ACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCG   | 2899 |



Qy 2902 TGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAG 2961  
 |||  
 Db 2900 TGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAG 2959

Qy 2962 TTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT 3021  
 |||  
 Db 2960 TTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT 3019

Qy 3022 TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGG 3081  
 |||  
 Db 3020 TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGG 3079

Qy 3082 ATTCAGAAAAGTCTTGTCTGAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAA 3141  
 |||  
 Db 3080 ATTCAGAAAAGTCTTGTCTGAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAA 3139

Qy 3142 AA 3143  
 ||  
 Db 3140 AA 3141

### RESULT 3

AY402621

LOCUS AY402621 2172 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY402621

VERSION AY402621.1 GI:39758607

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2172)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2172)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .2172

/organism="Homo sapiens"

/mol\_type="genomic DNA"

```

gene          /db_xref="taxon:9606"
              <1..>2172
              /locus_tag="HCM1285"
ORIGIN
Query Match      59.6%; Score 1874; DB 9; Length 2172;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1874; Conservative 0; Mismatches 298; Indels 0; Gaps 0;

Qy      105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
          |||
Db       1  ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 60

Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGGCCCATGCCC 224
          |||
Db       61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGGCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
          |||
Db      121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
          |||
Db      181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy      345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGTCCCCAGGC'TAAAGAACATG 404
          |||
Db      241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGTCCCCAGGC'TAAAGAACATG 300

Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
          |||
Db      301 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
          |||
Db      361 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 420

Qy      525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAAC'TTCAAGATTCCTAC 584
          |||
Db      421 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAAC'TTCAAGATTCCTAC 480

Qy      585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCTTTTGACCCC 644
          |||
Db      481 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCTTTTGACCCC 540

Qy      645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
          |||
Db      541 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 600

Qy      705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCC'TCAAGACC 764
          |||
Db      601 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCC'TCAAGACC 660

Qy      765 GACAAC'TTCC'TCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
          |||
Db      661 GACAAC'TTCC'TCCGCTGGCTGCATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

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|    |      |  |      |
|----|------|--|------|
| Qy | 825  | CAGGTCGTCTACTTCTTCTTCGAGGACAGCCAGCGAGTTTGACTTCTTTGAGAGGGCTC        | 884  |
| Db | 721  | NNN    | 780  |
| Qy | 885  | CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGC GGCGAAAAGCTGCTGCAG      | 944  |
| Db | 781  | NNN    | 840  |
| Qy | 945  | AAGAAGTGGACCACCTTCTCTGAAGGCC CAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC     | 1004 |
| Db | 841  | NNN    | 900  |
| Qy | 1005 | TTC AACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC       | 1064 |
| Db | 901  | NNN    | 960  |
| Qy | 1065 | TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGG ACCAGGAGCTCTGCGGTTTTGTGCC<br> | 1124 |
| Db | 961  | NNNNNNNNNNNNNNNNNNNNNNNGCAGGTTGGCGGG ACCAGGAGCTCTGCGGTTTTGTGCC     | 1020 |
| Qy | 1125 | TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA<br>   | 1184 |
| Db | 1021 | TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA       | 1080 |
| Qy | 1185 | ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA<br>   | 1244 |
| Db | 1081 | ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA       | 1140 |
| Qy | 1245 | GTGGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAG<br>    | 1304 |
| Db | 1141 | GTGGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAG        | 1200 |
| Qy | 1305 | CAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCA GTG<br>   | 1364 |
| Db | 1201 | CAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCA GTG       | 1260 |
| Qy | 1365 | GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA<br>   | 1424 |
| Db | 1261 | GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA       | 1320 |
| Qy | 1425 | GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT<br>   | 1484 |
| Db | 1321 | GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT       | 1380 |
| Qy | 1485 | CAGCTGTTCCCTGACCCTGAACCTGTT CGCAACCTGCAGCTGGCCCCCACCCAGGGTGCA<br>  | 1544 |
| Db | 1381 | CAGCTGTTCCCTGACCCTGAACCTGTT CGCAACCTGCAGCTGGCCCCCACCCAGGGTGCA      | 1440 |
| Qy | 1545 | GTGTTTG TAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCA ACTGTAGTGTCTAT<br> | 1604 |
| Db | 1441 | GTGTTTG TAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCA ACTGTAGTGTCTAT     | 1500 |
| Qy | 1605 | GAGAGCTGTGTGGACTGTGT CCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC<br>  | 1664 |
| Db | 1501 | GAGAGCTGTGTGGACTGTGT CCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC      | 1560 |
| Qy | 1665 | CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCCTGGAAGCAGGACATGGAGCGG       | 1724 |

|    |      |   |      |
|----|------|---|------|
|    |      |   |      |
| Db | 1561 | CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG   | 1620 |
| Qy | 1725 | GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC  | 1784 |
|    |      |   |      |
| Db | 1621 | GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC  | 1680 |
| Qy | 1785 | CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC   | 1844 |
|    |      |   |      |
| Db | 1681 | CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC   | 1740 |
| Qy | 1845 | CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA  | 1904 |
|    |      |   |      |
| Db | 1741 | CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA  | 1800 |
| Qy | 1905 | GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT  | 1964 |
|    |      |   |      |
| Db | 1801 | GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT  | 1860 |
| Qy | 1965 | CTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG  | 2024 |
|    |      |   |      |
| Db | 1861 | CTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG  | 1920 |
| Qy | 2025 | GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT   | 2084 |
|    |      |   |      |
| Db | 1921 | GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT   | 1980 |
| Qy | 2085 | GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCTAC   | 2144 |
|    |      |   |      |
| Db | 1981 | GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCTAC   | 2040 |
| Qy | 2145 | TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC   | 2204 |
|    |      |   |      |
| Db | 2041 | TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC   | 2100 |
| Qy | 2205 | ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG | 2264 |
|    |      |   |      |
| Db | 2101 | ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG | 2160 |
| Qy | 2265 | ACCCTGCGCCCT  | 2276 |
|    |      |   |      |
| Db | 2161 | ACCCTGCGCCCT  | 2172 |

# RESULT 4

AY402622

LOCUS AY402622 2133 bp DNA linear GSS 12-DEC-2003  
 DEFINITION Pan troglodytes HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY402622

VERSION AY402622.1 GI:39758608

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 2133)



|    |      |                  |                   |                   |                   |      |
|----|------|------------------|-------------------|-------------------|-------------------|------|
| Db | 361  | GAGACACAGTGTTC   | CAACTTCATCCGTG    | TCCTGGTTTCTTACA   | ATGTCACCCATCTCTAC | 420  |
| Qy | 525  | ACCTGCGGCACCTTC  | GCCTTCAGCCCTGCTT  | GTACCTTCATTGAACTT | CAAGATTCTCTAC     | 584  |
|    |      |                  |                   |                   |                   |      |
| Db | 421  | ACCTGCGGCACCTTC  | GCCTTCAGCCCTGCTT  | GTACCTTCATTGAACTT | CAAGATTCTCTAC     | 480  |
| Qy | 585  | CTGTTGCCCATCTCG  | GAGGACAAGGTCATGG  | AGGGGAAAAGGCCAA   | AGCCCCTTTGACCCC   | 644  |
|    |      |                  |                   |                   |                   |      |
| Db | 481  | CTGTTGCCCATCTCG  | GAGGACAAGGTCATGG  | AGGGGAAAAGGCCAA   | AGCCCCTTTGACCCC   | 540  |
| Qy | 645  | GCTCACAAGCATACG  | GCTGTCTTGGTGGAT   | GGGATGCTCTATTCT   | GGTACTATGAACAAC   | 704  |
|    |      |                  |                   |                   |                   |      |
| Db | 541  | GCTCACAAGCATACG  | GCTGTCTTGGTGGNN   | NNNNNNNNNNNNNNNN  | NNNNNNNNNNNNNNNN  | 600  |
| Qy | 705  | TTCTGGGCAGTGAGCC | CCTGATGCGCACACTGG | GATCCCAGCCTGTCTC  | CAAGACC           | 764  |
|    |      |                  |                   |                   |                   |      |
| Db | 601  | NTCTGGGCAGTGAGCC | CCTGATGCGCACACTGG | GATCCCAGCCTGTCTC  | CAAGACC           | 660  |
| Qy | 765  | GACAACTTCCTCCGCT | GGCTGCATCATGACGC  | CTCCTTTGTGGCAGCC  | ATCCCTTCGACC      | 824  |
|    |      |                  |                   |                   |                   |      |
| Db | 661  | GACAACTTCCTCCGCT | GGCTGCATC         | NNNNNNNNNNNNNNNN  | NNNNNNNNNNNNNNNN  | 720  |
| Qy | 825  | CAGGTCGTCTACTTCT | TCTTCGAGGAGACAGCC | AGCGAGTTTGACTTCT  | TTGAGAGGCTC       | 884  |
| Db | 721  | NNNNNNNNNNNNNNNN | NNNNNNNNNNNNNNNN  | NNNNNNNNNNNNNNNN  | NNNNNNNNNNNNNNNN  | 780  |
| Qy | 885  | CACACATCGCGGGTGG | CTAGAGTCTGCAAGAAT | GACGTGGGCGGCGAAA  | AGCTGCTGCAG       | 944  |
| Db | 781  | NNNNNNNNNNNNNNNN | NNNNNNNNNNNNNNNN  | NNNNNNNNNNNNNNNN  | NNNNNNNNNNNNNNNN  | 840  |
| Qy | 945  | AAGAAGTGGACCACCT | TCTTGAAGGCCAGCTG  | CTCTGCACCCAGCCGG  | GGCAGCTGCCC       | 1004 |
| Db | 841  | NNNNNNNNNNNNNNNN | NNNNNNNNNNNNNNNN  | NNNNNNNNNNNNNNNN  | NNNNNNNNNNNNNNNN  | 900  |
| Qy | 1005 | TTCAACGTCATCCGCC | ACGCGGTCTGCTCCCC  | GCCGATTCTCCCACAG  | CTCCCCACATC       | 1064 |
| Db | 901  | NNNNNNNNNNNNNNNN | NNNNNNNNNNNNNNNN  | NNNNNNNNNNNNNNNN  | NNNNNNNNNNNNNNNN  | 960  |
| Qy | 1065 | TACGCAGTCTTCACCT | CCCAGTGGCAGGTTGG  | CGGGACCAGGAGCTCT  | GCGGTTTGTGCC      | 1124 |
|    |      |                  |                   |                   |                   |      |
| Db | 961  | NNNNNNNNNNNNNNNN | NNNNNNNNNGCAGGTT  | GGCGGGACCAGGAGCT  | CTGCGGTTTGTGCC    | 1020 |
| Qy | 1125 | TTCTCTCTCTTGGAC  | ATTGAACGTGTCTTTA  | AGGGGAAATACAAAG   | AGTTGAACAAAGAA    | 1184 |
|    |      |                  |                   |                   |                   |      |
| Db | 1021 | TTCTCTCTCTTGGAC  | ATTGAACGTGTCTTTA  | AGGGGAAATACAAAG   | AGTTGAACAAAGAA    | 1080 |
| Qy | 1185 | ACTTCACGCTGGACTA | CTTATAGGGGCCCTG   | AGACCAACCCCCGGCC  | AGGCAGTTGCTCA     | 1244 |
|    |      |                  |                   |                   |                   |      |
| Db | 1081 | ACTTCACGCTGGACTA | CTTATAGGGGCCCTG   | AGACCAACCCCCGGCC  | AGGCAGTTGCTCA     | 1140 |
| Qy | 1245 | GTGGGCCCCCTCCTC  | TGATAAGGCCCTGACCT | TTCATGAAGGACCAT   | TTCTTGATGGATGAG   | 1304 |
|    |      |                  |                   |                   |                   |      |
| Db | 1141 | GTGGGCCCCCTCCTC  | TGATAAGGCCCTGACCT | TTCATGAAGGACCAT   | TTCTTGATGGATGAG   | 1200 |
| Qy | 1305 | CAAGTGGTGGGGACG  | CCCCCTGCTGGTGAAAT | CTGGCGTGGAGTATA   | CACGGCTTGCAAGTG   | 1364 |
|    |      |                  |                   |                   |                   |      |
| Db | 1201 | CAGGTGGTAGGGACG  | CCCCCTGCTGGTGAAAT | CTGGCGTGGAGTATA   | CACGGCTTGCAAGTG   | 1260 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1365 | GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA  | 1424 |
|    |      |   |      |
| Db | 1261 | GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA  | 1320 |
| Qy | 1425 | GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT  | 1484 |
|    |      |   |      |
| Db | 1321 | GGGTCGNTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGANNNNTT   | 1380 |
| Qy | 1485 | CAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCA  | 1544 |
|    |      |   |      |
| Db | 1381 | CAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCA  | 1440 |
| Qy | 1545 | GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTAT | 1604 |
|    |      |   |      |
| Db | 1441 | GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTAT | 1500 |
| Qy | 1605 | GAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGACCTTGAGTCC   | 1664 |
|    |      |   |      |
| Db | 1501 | GAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGATCCTGAGTCC   | 1560 |
| Qy | 1665 | CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG   | 1724 |
|    |      |   |      |
| Db | 1561 | CGAACCTGTTGCCTCCTNNNNNNNNNNNNNGAACTCCTGGAAGCAGGACATGGAGCGG    | 1620 |
| Qy | 1725 | GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC  | 1784 |
|    |      |   |      |
| Db | 1621 | GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC  | 1680 |
| Qy | 1785 | CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCTGC    | 1844 |
|    |      |   |      |
| Db | 1681 | CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGNTCCCTGC    | 1740 |
| Qy | 1845 | CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA  | 1904 |
|    |      |   |      |
| Db | 1741 | CCCCACCTGTCAGCCTTGGCCTCTTACTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA  | 1800 |
| Qy | 1905 | GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT  | 1964 |
|    |      |   |      |
| Db | 1801 | GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT  | 1860 |
| Qy | 1965 | CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG  | 2024 |
|    |      |   |      |
| Db | 1861 | CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG  | 1920 |
| Qy | 2025 | GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT   | 2084 |
|    |      |   |      |
| Db | 1921 | GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT   | 1980 |
| Qy | 2085 | GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTAC  | 2144 |
|    |      |   |      |
| Db | 1981 | GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTAC  | 2040 |
| Qy | 2145 | TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATC | 2204 |
|    |      |   |      |
| Db | 2041 | TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATC | 2100 |





REFERENCE 6 (bases 1 to 3206)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1..3206 /organism="Mus musculus" /mol\_type="mRNA" /strain="C57BL/6J" /db\_xref="FANTOM\_DB:6030492A12" /db\_xref="taxon:10090" /clone="6030492A12" /sex="male" /tissue\_type="testis" /clone\_lib="RIKEN full-length enriched mouse cDNA library" /dev\_stage="13 days embryo"

misc\_feature 224..2507 /note="putative sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A (MGD|MGI:107560, GB|NM\_013658, evidence: BLASTN, 99%, match=2517)"

polyA\_signal 3181..3186 /note="putative"

polyA\_site 3206 /note="putative"

ORIGIN

Query Match 55.6%; Score 1747.4; DB 3; Length 3206;  
 Best Local Similarity 76.7%; Pred. No. 0;  
 Matches 2355; Conservative 0; Mismatches 621; Indels 95; Gaps 14;

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 Db 194 GAACCATCTGGTGACCATCTCAGGCTGACCATGGCCCTACCATCCCTGGGCCAGGACTCA 253

Qy 135 TGGAGCCTCCTGGGCCTTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACC 194  
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 Db 254 TGGAGTCTCCTGCCGTGTTTTTTCTTCCAACCTCTTCTGCTGCCATCACTGCCACCTGCT 313

Qy 195 GCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGT 254  
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 Db 314 TCTGGGACTGGTGGTCAGGGGCCCATGCCCAGAGTCAAATACCATGCTGGAGACGGGCAC 373

Qy 255 AGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGT 314  
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 Db 374 AGGGCCCTCAGCTTCTTCCAACAAAAAGGCCTCCGAGACTTTGACACGCTGCTCCTGAGT 433

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 Db 434 GACGATGGCAACACTCTCTATGTGGGGGCTCGAGAGGCCGTCTTGGCCTTGAATATCCAG 493

Qy 375 GATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAG 434  
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 Db 494 AACCAGGAATCCCAAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGAGAGAAAAAAG 553

Qy 435 AGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTC 494  
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 Db 554 ACCGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATTCGAGTC 613

Qy 495 CTGGTTTCTTACAATGTCAACCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCT 554  
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 Db 614 CTGGTCTCTTACAATGCTACTCACCTCTATGCCTGTGGGACCTTTGCCTTCAGCCCTGCC 673

Qy 555 TGTACCTTCATTGAACTTCAAGATTCCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATG 614  
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 Db 674 TGTACCTTCATTGAACTCCAAGATTCCCTCCTGTTGCCCATCTTGATAGACAAGGTCATG 733

Qy 615 GAGGGAAAAGGCCAAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGAT 674  
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 Db 734 GACGGGAAGGGCCAAAAGCCCCTTTGACCCCTGTTTCAAGCACACAGCTGTCTTGGTCGAT 793

Qy 675 GGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGC 734  
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 Db 794 GGGATGCTTTATTCCGGCACCATGAACAACTTCCTGGGCAGCGAGCCCATCCTGATGCGG 853

Qy 735 ACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGAC 794  
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 Db 854 ACACTGGGATCCCAGCCTGTTCTCAAGACTGACATCTTCTTACGCTGGCTGCACGCGGAT 913

Qy 795 GCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACA 854  
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 Db 914 GCCTCCTTCGTGGCAGCCATTCCATCCACCCAGGTCGTCTATTTCTTCTTTGAGGAGACA 973

Qy 855 GCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAG 914  
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 Db 974 GCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGGTGGCTCAAGTCTGCAAG 1033

Qy 915 AATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAG 974

|    |      |  |      |
|----|------|--|------|
| Db | 1034 | AACGACGTGGGCGGTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTCAAAGCCCAG   | 1093 |
| Qy | 975  | CTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTC    | 1034 |
| Db | 1094 | TTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCCGCCACGCGGTCTGCTG    | 1153 |
| Qy | 1035 | CCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTT    | 1094 |
| Db | 1154 | CCCGCCGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCCCAGTGGCAGGTT   | 1213 |
| Qy | 1095 | GGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTT   | 1154 |
| Db | 1214 | GGCGGGACCAGGAGCTCAGCAGTCTGTGCCTTCTCTCTCACGGACATTGAGCGAGTCTTT   | 1273 |
| Qy | 1155 | AAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCT    | 1214 |
| Db | 1274 | AAAGGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCGGGGCTCA   | 1333 |
| Qy | 1215 | GAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACC  | 1274 |
| Db | 1334 | GAGGTCAGCCCGAGGCAAGGCAGTTGCTCCATGGGCCCCCTCCTCTGACAAAGCCTTGACC  | 1393 |
| Qy | 1275 | TTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAA  | 1334 |
| Db | 1394 | TTCATGAAGGACCATTTCCTGATGGATGAGCACGTGGTAGGAACACCCCTGCTGGTGAAAG  | 1453 |
| Qy | 1335 | TCTGGCGTGAGGTATACACGGCTTGACAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGC  | 1394 |
| Db | 1454 | TCTGGTGTGGAGTACACACGGCTTGCTGTGGAGTCAGCTCGGGGCCTTGATGGGAGCAGC   | 1513 |
| Qy | 1395 | CATCTTGTGATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGG   | 1454 |
| Db | 1514 | CATGTGGTGCATGTATCTGGGTACCTCCACGGGGTCCCTGCACAAGGCTGTGGTGCCTCAG  | 1573 |
| Qy | 1455 | GACAGCAGTGCTCATCTGGTGGAGAGATTGAGCTG-TTCCCTGACCCTGAACCTGTTCTG   | 1513 |
| Db | 1574 | GACAGCAGTGCTTATCTCGTGGAGGAGATTGAGCTGAGCCCCCTGACTCTGAGCCTGTTCTG | 1633 |
| Qy | 1514 | CAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTG    | 1573 |
| Db | 1634 | AAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGTTTGCAGGCTTCTCTGGAGGCATCTG    | 1693 |
| Qy | 1574 | GAGGGTGGCCCGAGCCAATTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCG    | 1633 |
| Db | 1694 | GAGAGTCCCAGGGCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCCAG    | 1753 |
| Qy | 1634 | GGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAA   | 1693 |
| Db | 1754 | GGACCCCTCACTGTGCCTGGGACCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTCTAC  | 1813 |
| Qy | 1694 | CCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGG   | 1753 |
| Db | 1814 | C---AAGCCTTGAAGCAGGACATGGAACGCGGCAACCCGAGTGGGTATGCACCCGTGG     | 1870 |
| Qy | 1754 | CCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGC    | 1813 |

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|----|------|---|------|
| Db | 1871 | CCCCATGGCCAGGAGCCCCCGCGCTCAGAGCCCCCTCAACTAATTAAAGAAGTCCCTGAC  | 1930 |
| Qy | 1814 | TGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTA   | 1873 |
|    |      |   |      |
| Db | 1931 | AGTCCCCAACTCCATCCTGGAGCTGCCCTGCCCCACCTGTCAGCACTGGCCTCTTACCA   | 1990 |
| Qy | 1874 | TTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT  | 1933 |
|    |      |   |      |
| Db | 1991 | CTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGGCTCCCT  | 2050 |
| Qy | 1934 | CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGTCTGGGCAACTGAGAATGG | 1993 |
|    |      |   |      |
| Db | 2051 | CTTGCTGCTGCCGAGGATGGTGTCTGGAGGCCCTTACCAGTGTGTGGCGACTGAGAACGG  | 2110 |
| Qy | 1994 | CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCCTGGCCCTGGA | 2053 |
|    |      |   |      |
| Db | 2111 | CTACTCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCCCTGGCGCTGGA | 2170 |
| Qy | 2054 | TCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGTCCCGTTGACCAGGGTCAGTGG    | 2113 |
|    |      |   |      |
| Db | 2171 | CCCTGAGCTGGCGGGCGTTCCCCGTGAGCGTGTGCAGTCCCGCTGACCAGGGTCGGAGG   | 2230 |
| Qy | 2114 | TGGGGCCGCCCTGGCTGCCAGCAGTCCCTACTGGCCCCACTTTTGTCACTGTCACTGTCT  | 2173 |
|    |      |   |      |
| Db | 2231 | CGGAGCTTCCATGGCTGCCAGCGGTCCCTACTGGCCCCATTTTCTCATCGTTACCGTCT   | 2290 |
| Qy | 2174 | CTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT  | 2233 |
|    |      |   |      |
| Db | 2291 | CCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCACTGGGGGCGCT  | 2350 |
| Qy | 2234 | CCGGGCTCGGGGAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTT  | 2293 |
|    |      |   |      |
| Db | 2351 | GCGGGCTCGGGGTAAGGTTTCAGGGCTGTGGGATGCTGCCCCCAGGGAAAAGGCTCCACT  | 2410 |
| Qy | 2294 | AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA  | 2353 |
|    |      |   |      |
| Db | 2411 | GAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGACGTAGA  | 2470 |
| Qy | 2354 | CGCTGACAACAACTGCCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCT- | 2412 |
|    |      |   |      |
| Db | 2471 | TGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAGATCCGCAGCTG  | 2530 |
| Qy | 2413 | -GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGGCCAAGCACAGCCCTGACTAGGATG  | 2471 |
|    |      |   |      |
| Db | 2531 | AGCAGAGCAAGCCACTGGCCTTGT'TGGCTATGC-----                       | 2563 |
| Qy | 2472 | ACAGCAGCACAAAAGACCACCTTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACT | 2531 |
|    |      |   |      |
| Db | 2564 | ----CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAACGTGTGTCACC  | 2619 |
| Qy | 2532 | GATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCATGGGACTCCCTTCTACC   | 2591 |
|    |      |   |      |
| Db | 2620 | TACAGCACCCAGTAGG-----TCCTCCCCGTGGGACTCTCTTCTGCA               | 2662 |
| Qy | 2592 | AAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATAT  | 2651 |
|    |      |   |      |
| Db | 2663 | AGCACATTGGGCTGTCT-----CCATACCTGTACTTGTGCTGTGAC                | 2703 |

Qy 2652 TGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAG 2711  
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 Db 2704 AGGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTCCTGTAACAAAC 2763  
 Qy 2712 TGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAA 2771  
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 Db 2764 GTGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGACAAAC-CTAAG 2822  
 Qy 2772 CATCTAAACAATCATATGCTA-----ACATGCCACTCCTGGAAACTCCACTCT----G 2820  
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 Db 2823 CATCCGAGCAAGCTGGGGCTATTCTGCAAACTCCATCCTGAACGCTGTCACCTCTAGAAG 2882  
 Qy 2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAGGGATCTGCTCC 2879  
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 Db 2883 CAGCTGCTGCTTTGAACACCAGCCACCCTCCTTCCCAAGAGTCTCTATGGAGTTGGCCC 2942  
 Qy 2880 CTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTG 2939  
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 Db 2943 CTTGTGTTTCCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTA 2999  
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 Db 3000 ACCACCTTCCTTCTTGCTTCAGTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAG 3059  
 Qy 2996 AATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCT 3055  
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 Db 3060 AATGGGGGGCATAATCTGAGCCTTGTTCCCTTGTCAGTGTGGCTGACCCTTGACCTCTT 3119  
 Qy 3056 CCCCTCCCTTTTCCCTTTGTTTGGGATTTCAGAAAACCTGCTTGTGACAGACTGTTTATTT 3115  
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 Db 3120 --CCTTCCTCCTCCCTTTGTTTGGGATTTCAGAAAACCTGCTTGTGACAGACAATTTATTT 3177  
 Qy 3116 TTTATTAAAAA 3126  
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 Db 3178 TTTATTAAAAA 3188

# RESULT 6

AK035918

LOCUS AK035918 3086 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630018D15 product:sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A, full insert sequence.

ACCESSION AK035918

VERSION AK035918.1 GI:26084904

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3086)  
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:<http://genome.gsc.riken.jp/>  
 URL:<http://fantom.gsc.riken.jp/>.

FEATURES  
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 /organism="Mus musculus"  
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 /note="putative"  
 polyA\_site 3086  
 /note="putative"

#### ORIGIN

Query Match 54.1%; Score 1701.4; DB 3; Length 3086;  
 Best Local Similarity 75.2%; Pred. No. 0;  
 Matches 2364; Conservative 0; Mismatches 637; Indels 141; Gaps 14;

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|    |     |   |     |
| Db | 4   | AACCCAGAAAGTGCCTGTTTCCTCAGAACCATCTGGTGACCATCTCAGGCTGACCATGGC  | 63  |
| Qy | 110 | CCTCCCAGCCCTGGGCTGGACCCCTGGAGCCTCCTGGGCCCTTTTCCTCTTCCAACCTGCT | 169 |
|    |     |   |     |
| Db | 64  | CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTCTTCCAACCTCTT   | 123 |
| Qy | 170 | TCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCAGGGT    | 229 |
|    |     |   |     |
| Db | 124 | CCTGCTGCCATCAC TGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCAGAGT  | 183 |
| Qy | 230 | CAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCA  | 289 |
|    |     |   |     |
| Db | 184 | CAAATACCATGCTGGAGACGGGCACAGGGCCCTCAGCTTCTTCCAACAAAAGGCCTCCG   | 243 |
| Qy | 290 | GGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGA  | 349 |
|    |     |   |     |
| Db | 244 | AGACTTTGACACGCTGCTCCTGAGTGACGATGGCAACACTCTCTATGTGGGGGCTCGAGA  | 303 |
| Qy | 350 | AGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACC  | 409 |
|    |     |   |     |
| Db | 304 | GGCCGTCCTGGCCTTGAATATCCAGAACCAGGAATCCCAAGGCTAAAGAACATGATACC   | 363 |
| Qy | 410 | GTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGAC   | 469 |

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|----|------|--|------|
| Db | 364  | <br>CTGGCCAGCCAGTGAGAGAAAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAATGAGAC   | 423  |
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| Db | 424  | <br>ACAGTGTTTCAACTTCATTCGAGTCCCTGGTCTCTTACAATGCTACTCACCTCTATGCCCTG | 483  |
| Qy | 530  | CGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATT-----                         | 566  |
| Db | 484  | <br>TGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTACGTGCGACCCTGGCATTCTGGG   | 543  |
| Qy | 567  | -----GAACTTCAAGATTCCCTACCTGTTGCCCATCTCGGAG                         | 602  |
| Db | 544  | <br>CTCCCAGCCTCTTCCCCCCTCTAGGAACTCCAAGATTCCCTCCTGTTGCCCATCTTGATA   | 603  |
| Qy | 603  | GACAAGGTCATGGAGGGAAAAGGCCAAAGCCCTTTGACCCGCTCACAAGCATACGGCT         | 662  |
| Db | 604  | <br>GACAAGGTCATGGACGGGAAGGCCAAAGCCCTTTGACCCTGTTCAACAAGCACACAGCT    | 663  |
| Qy | 663  | GTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCCTGGGCAGTGAGCCC      | 722  |
| Db | 664  | <br>GTCTTGGTCGATGGGATGCTTTATTCCGGCACCATGAACAACCTTCCTGGGCAGCGAGCCC  | 723  |
| Qy | 723  | ATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACCTTCCTCCGCTGG      | 782  |
| Db | 724  | <br>ATCCTGATGCGGACACTGGGATCCCAGCCTGTTCTCAAGACTGACATCTTCTTACGCTGG   | 783  |
| Qy | 783  | CTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTC       | 842  |
| Db | 784  | <br>CTGCACGCGGATGCCTCCTTCGTGGCAGCCATTCCATCCACCCAGGTCGTCTATTTCTTC   | 843  |
| Qy | 843  | TTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGGCT        | 902  |
| Db | 844  | <br>TTTGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGTGGCT    | 903  |
| Qy | 903  | AGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC       | 962  |
| Db | 904  | <br>CAAGTCTGCAAGAACGACGTGGGCGGTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC   | 963  |
| Qy | 963  | CTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCAC       | 1022 |
| Db | 964  | <br>CTCAAAGCCCAGTTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCCGCCAC   | 1023 |
| Qy | 1023 | GCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCC       | 1082 |
| Db | 1024 | <br>GCGGTCCTGCTGCCCGCCGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCC   | 1083 |
| Qy | 1083 | CAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTGGACATT        | 1142 |
| Db | 1084 | <br>CAGTGGCAGGTTGGCGGGACCAGGAGCTCAGCAGTCTGTGCCTTCTCTCTCACGGACATT   | 1143 |
| Qy | 1143 | GAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACT        | 1202 |
| Db | 1144 | <br>GAGCGAGTCTTTAAAGGGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACT  | 1203 |
| Qy | 1203 | TATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGGCCCTCCTCTGAT       | 1262 |
|    |      | <br>   |      |



Db 1204 TACCGGGGCTCAGAGGTCAGCCCCAGGCCAGGCAGTTGCTCCATGGGCCCCCTCCTCTGAC 1263

Qy 1263 AAGGCCCTGACCTTCATGAAGGACCATTTCTCTGATGGATGAGCAAGTGGTGGGGACGCCC 1322  
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Db 1264 AAAGCCTTGACCTTCATGAAGGACCATTTCTCTGATGGATGAGCACGTGGTAGGAACACCC 1323

Qy 1323 CTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCCAGGGCCTT 1382  
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Db 1324 CTGCTGGTGAACTCTGGTGTGGAGTACACACGGCTTGCTGTGGAGTCAGCTCGGGGCCTT 1383

Qy 1383 GATGGGCACAGCCATCTTGTCTGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCT 1442  
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Db 1384 GATGGGAGCAGCCATGTGGTCTGTATCTGGGTACCTCCACGGGGTCCCTGCACAAGGCT 1443

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Db 1444 GTGGTGCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTGAGCTGAGCCCTGACTCT 1503

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Qy 1683 TCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGAACCCAGAGTGGGCA 1742  
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Db 1684 TCTGGCTCTACC---AAGCCTTGGAAGCAGGACATGGAACGCGGCAACCCGGAGTGGGTA 1740

Qy 1743 TGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1802  
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Db 1741 TGCACCCGTGGCCCCATGGCCAGGAGCCCCGGCGTCAGAGCCCCCTCAACTAATTA 1800

Qy 1803 GAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTG 1862  
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Db 1801 GAAGTCCTGACAGTCCCCAACTCCATCCTGGAGCTGCCCTGCCCCACCTGTCAGCACTG 1860

Qy 1863 GCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTAC 1922  
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Db 1861 GCCTCTTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTAC 1920

Qy 1923 AATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGTGGGCA 1982  
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Db 2041 CTGGCGCTGGACCCTGAGCTGGCGGGCGTTCCCCGTGAGCGTGTGCAGGTCCCCTGACC 2100

Qy 2103 AGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCTACTGGCCCCACTTTGTCACT 2162  
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 Qy 2223 TTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCGTGCGCCCTGGGGAG 2282  
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 Db 2221 CTGGGGGCGCTGCGGGCTCGGGGTAAGGTTTCAGGGCTGTGGGATGCTGCCCCCAGGGAA 2280  
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 Db 2341 AGTGACGTAGATGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAG 2400  
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 Db 2445 -----CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAA 2489  
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 Db 2490 CGTGTGTACCTACAGCACCCAGTAGGT-----CCTCCCCTGTGGGAC 2532  
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 Db 2634 CTGTAACAAACGTGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCCTGTGGTGA 2693  
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 Db 2694 CAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCCCTGCAAACCTCCATCCTGAACGCTGT 2752  
 Qy 2814 CACTCT----GAAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAG 2868  
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 Db 2753 CACTCTAGAAGCAGCTGCTGCTTTGAACACCAGCCACCTCCTTCCCAAGAGTCTCTAT 2812  
 Qy 2869 GGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTT 2928  
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 Db 2813 GGAGTTGGCCCCTTGTGTTTCCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATC 2869



Query Match 43.7%; Score 1372.2; DB 9; Length 2172;  
Best Local Similarity 71.9%; Pred. No. 0;  
Matches 1560; Conservative 0; Mismatches 611; Indels 0; Gaps 0;

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Qy      105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCCTTTTCCTCTTCCAA 164
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Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 224
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Db      61 CTCTTCCTGCTGCCATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCCTTAGCTTCTTCCACCAGAAGGGC 284
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Db     121 AGAGTCAAATACCATGCTGGAGACGGGCACAGGGCCCTCAGCTTCTTCCAACAAAAAGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
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Qy      345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG 404
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Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
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Db     301 ATACCCTGGCCAGCCAGTGAGAGAAAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTTCAACTTCATCCGTGTCTTGGTTTCTTACAATGTCAACCATCTCTAC 524
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy      525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC 584
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Qy      585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC 644
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Db     481 CTGTTGCCCATCTTGATAGACAAGGTCATGGACGGGAAGGGCCAAAGCCCCTTTGACCCCT 540

Qy      645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
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Db     541 GTTCAACAAGCACACAGCTGTCTTGGTCGATGGGATGCTTTATTCGGGCACCATGAACAAC 600

Qy      705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACC 764
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Db     601 TTCCTGGGCAGCGAGCCCATCCTGATGCGGACACTGGGATCCCAGCCTGTCTCAAGACT 660

Qy      765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
          |||| |||| | ||||| |||||
Db     661 GACATCTTCTTACGCTGGCTGCACGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

Qy      825 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 884

Db     721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780

Qy      885 CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGGCGAAAAGCTGCTGCAG 944
```

[illegible]



Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 907.f  
 For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?s=CS0AL002BH02NP1&c=907.f>.

FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
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 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

#### ORIGIN

Query Match 30.2%; Score 950.6; DB 5; Length 1108;  
 Best Local Similarity 94.8%; Pred. No. 4.1e-240;  
 Matches 996; Conservative 24; Mismatches 27; Indels 4; Gaps 4;

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| Qy | 2073 | CCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCC  | 2132 |
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| Db | 1049 | CCCCGGGAGCATGT-AAGGTCCCGTTGACMAGGGTCAGTGG-KGGGCSGCCCTGGCTGCC  | 992  |
| Qy | 2133 | CAGCAGTCCTACTGGCCCC-ACTTTGTCACTGTCACTGTCTTTGCCTTAGTGCTTTC     | 2191 |
|    |      | :    :  |      |
| Db | 991  | CAGMAGTCMYACTTGCCCCAACTTTGTAACTGTAACGTCTCTTTGCCCTAAGTGCTTTC   | 932  |
| Qy | 2192 | AGGAGCCCTCATCATCCTCGTGGCCTCCCC-ATTGAGAGCACTCCGGGCTCGGGGCAAGG  | 2250 |
|    |      | :      :      :   |      |
| Db | 931  | AGGAGCCCTCATCATCCTCGTGGCCTCCCCAATTGAGAGMACTCCGGGCTCGGCACAAGG  | 872  |
| Qy | 2251 | TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACC  | 2310 |
|    |      | :      :      :      :  |      |
| Db | 871  | TTMAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACC  | 812  |
| Qy | 2311 | TCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCC | 2370 |
|    |      | :      :      :   |      |
| Db | 811  | TCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTAACAACAACCTGCC | 752  |
| Qy | 2371 | TAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGC  | 2430 |
|    |      | :      :      :   |      |
| Db | 751  | TAGGCACTGAGGTMGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGC  | 692  |
| Qy | 2431 | CATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCA  | 2490 |
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Db 691 CATGCTGGCTGGGCGGCCCAAGMACAGCCCTGACTAGGATSACAGCAGCACAAAAGACCA 632  
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 Db 511 CAGGGTGGGGGCTACCCCCAGACCTGCTCCTAAACTGATATTGAAGAACCTGGAGAGGAT 452  
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 Db 451 CCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAA 392  
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 Db 331 TAAMATGCAACTCCTGGAAACTCMAMTCTGAAGCTGCCGCTTTGAAMACCAAACCTCCCT 272  
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 Db 271 TCTCCCAGGGTCATGMAGGGATCTGCTCCCTCCTGCTTCCCTTACMAGTCGTGMACAGCT 212  
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 Db 211 AACTCCCAGGAAGTCTTCCCTGAAGTCTGACCACCTTTCNTCTAGCTTAAGTTGGRGAAA 152  
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 Db 151 ACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATNTGAGCCTTCTTAACTCCTT 92  
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 Qy 3091 ACTGCTTGTCAGAGACTGTTTATTTTTTATT 3121  
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 Db 31 ACTGCTTGTCAGAGACTGTTTCBYTTTTCTT 1

# RESULT 9

BX363741/c

LOCUS BX363741 1064 bp mRNA linear EST 23-APR-2004

DEFINITION BX363741 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
Homo sapiens cDNA clone CS0DL005YC17 3-PRIME, mRNA sequence.

ACCESSION BX363741

VERSION BX363741.2 GI:46554166

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens



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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1064)
AUTHORS        Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished (2001)
COMMENT        On May 5, 2003 this sequence version replaced gi:30384744.
                Contact: Genoscope
                Genoscope - Centre National de Sequencage
                2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
                end enriched, double-strand cDNA was digested with Not I and cloned
                into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
                was normalized. Library was constructed by Life Technologies, a
                division of Invitrogen. This sequence belongs to sequence cluster
                907.f
                For more information about this cluster, see
                http://www.genoscope.cns.fr/cdna?s=CS0DL005AB09NP1&c=907.f.
FEATURES
    source      1. .1064
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                25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match      29.5%; Score 926.2; DB 5; Length 1064;
Best Local Similarity 95.5%; Pred. No. 1.2e-233;
Matches 1000; Conservative 15; Mismatches 24; Indels 8; Gaps 6;

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Qy      2118  GCCGCCCTGGCTGCCCAGCAGTCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTT 2177
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Db      981  --CCGCCCTGGYGCCAGCAGTCCWAYTG--CCCCATTTGTCACTGTCACTGTCTCTTT 926

Qy      2178  GCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGG 2237
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Db      925  GCCTTAGTGCTTTCA-GAGCCCTCATCATCCTCGT-GCCTCCCCATTGAGAGCACTCCGG 868

Qy      2238  GCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGC 2297
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Qy      2298  AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT 2357
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|    |      |  |      |
|----|------|--|------|
| Db | 807  | AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT | 748  |
| Qy | 2358 | GACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT | 2417 |
|    |      |  |      |
| Db | 747  | GACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT | 688  |
| Qy | 2418 | GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA | 2477 |
|    |      |  |      |
| Db | 687  | GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA | 628  |
| Qy | 2478 | GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC | 2537 |
|    |      |  |      |
| Db | 627  | GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC | 568  |
| Qy | 2538 | ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC | 2597 |
|    |      |  |      |
| Db | 567  | ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC | 508  |
| Qy | 2598 | ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA | 2657 |
|    |      |  |      |
| Db | 507  | ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA | 448  |
| Qy | 2658 | ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC | 2717 |
|    |      |  |      |
| Db | 447  | ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC | 388  |
| Qy | 2718 | AAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA | 2777 |
|    |      |  |      |
| Db | 387  | AAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA | 328  |
| Qy | 2778 | AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC | 2837 |
|    |      |  |      |
| Db | 327  | AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC | 268  |
| Qy | 2838 | ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA | 2897 |
|    |      |  |      |
| Db | 267  | ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA | 208  |
| Qy | 2898 | GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCT | 2957 |
|    |      |  |      |
| Db | 207  | GTCGTGCACCGCTGACTYCCAGGAAGTCTTCCCTGAAKTCTGACCACCTTTCTTCTTGCT | 148  |
| Qy | 2958 | TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG-CAGGGGTAATCTGAGC | 3016 |
|    |      |  |      |
| Db | 147  | TCAGTTGGGGCAGAYTYTGATCCCTTCTGCCCTGGYAGAATGGTCAGGGGTAATCTGAGC | 88   |
| Qy | 3017 | CTTCTTCACTCCCTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTT | 3076 |
|    |      |  |      |
| Db | 87   | CTTCTTCACTCCCTTACCCTAGCTGACCCCTTCMCCTCTCCCBTSSCTTTTCCTTTGTT  | 28   |
| Qy | 3077 | TTGGGATTCAGAAAACCTGCTTGTGAGA                                 | 3103 |
|    |      |  |      |
| Db | 27   | TTGGGATTCAGAAAACCTGCTTGTGAGA                                 | 1    |

LOCUS BX350606 922 bp mRNA linear EST 08-APR-2004  
DEFINITION BX350606 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
Homo sapiens cDNA clone CS0DL005YC17 3-PRIME, mRNA sequence.

ACCESSION BX350606

VERSION BX350606.1 GI:30373499

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 922)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
907.f

For more information about this cluster, see

[http://www.genoscope.cns.fr/cdna?s=CS0BAI043ZD06\\_CS04076\\_1&c=907.f](http://www.genoscope.cns.fr/cdna?s=CS0BAI043ZD06_CS04076_1&c=907.f).

FEATURES Location/Qualifiers

source

1. .922

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DL005YC17"

/cell\_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"

/cell\_line="RAMOS CELL LINE"

/clone\_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT  
25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 27.8%; Score 874.4; DB 5; Length 922;

Best Local Similarity 98.7%; Pred. No. 6.1e-220;

Matches 878; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1372 CCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGC 1431  
||||| ||||||||||||||||||||||||||||||| ||||||| |||||||

Db 919 CCCAGGNCCTTGATGGGCACAGCCATCTTGTCATGTACTTGGGAACCACAACAGGGTCGC 860

Qy 1432 TCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGGAAGAGATTTCAGCTGT 1491  
||||| ||||||||||||||||||||||||||||||| ||||||| |||||||

Db 859 TCCACAAGACTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGGAAGAGATTTCAGCTGT 800

Qy 1492 TCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTTG 1551  
||||| ||||||||||||||||||||||||||||||| ||||| |||||||

Db 799 TCCCTGACCCTGANCTGTTTCGCAACCTGCAGCTGGCCNCCACCAAGGGTGCAGTGTTGN 740

|    |      |   |      |
|----|------|---|------|
| Qy | 1552 | TAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCT  | 1611 |
|    |      |   |      |
| Db | 739  | TAGGCTTCTCAGNAGGTGTCTGGAGGGTGCNCCGAGCCAACTGTAGTGTCTATGAGAGCT  | 680  |
| Qy | 1612 | GTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCT  | 1671 |
|    |      |   |      |
| Db | 679  | GTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCT  | 620  |
| Qy | 1672 | GTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACC   | 1731 |
|    |      |   |      |
| Db | 619  | GTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACC   | 560  |
| Qy | 1732 | CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC  | 1791 |
|    |      |   |      |
| Db | 559  | CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC  | 500  |
| Qy | 1792 | AAATCATTAAGAAGTCCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACC   | 1851 |
|    |      |   |      |
| Db | 499  | AAATCATTAAGAAGTCCCTGGCTGTCCCTAACTCCATCCTGGAGCTCCCCTGCCCCACC   | 440  |
| Qy | 1852 | TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT  | 1911 |
|    |      |   |      |
| Db | 439  | TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT  | 380  |
| Qy | 1912 | CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC  | 1971 |
|    |      |   |      |
| Db | 379  | CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC  | 320  |
| Qy | 1972 | AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC  | 2031 |
|    |      |   |      |
| Db | 319  | AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC  | 260  |
| Qy | 2032 | AGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGG   | 2091 |
|    |      |   |      |
| Db | 259  | AGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGG   | 200  |
| Qy | 2092 | TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCCTACTGGCCCC | 2151 |
|    |      |   |      |
| Db | 199  | TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCCTACTGGCCCC | 140  |
| Qy | 2152 | ACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCG  | 2211 |
|    |      |   |      |
| Db | 139  | ACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCG  | 80   |
| Qy | 2212 | TGGCCTCCCCATTGAGAGCACTCCGGGGCTCGGGGCAAGGTTTCAGGGCTGT          | 2261 |
|    |      |   |      |
| Db | 79   | TGGCCTCCCCATTGAGAGCACTCCGGGGCTCGGGGCAAGGTTTCAGGGCTGT          | 30   |

RESULT 11

BX384966

LOCUS BX384966 934 bp mRNA linear EST 23-APR-2004

DEFINITION BX384966 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.

ACCESSION BX384966

VERSION BX384966.2 GI:46556002

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 934)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30436505.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
907.f  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?s=CS0DL005AB09QP1&c=907.f>.

FEATURES Location/Qualifiers

source 1. .934  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DL005YC17"  
/cell\_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"  
/cell\_line="RAMOS CELL LINE"  
/clone\_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT  
25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

# ORIGIN

Query Match 27.0%; Score 849.2; DB 5; Length 934;  
Best Local Similarity 97.0%; Pred. No. 2.9e-213;  
Matches 871; Conservative 4; Mismatches 22; Indels 1; Gaps 1;

Qy 99 CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC 158  
|||||

Db 1 CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC 60

Qy 159 TTCCAAC TGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCC 218  
|||||

Db 61 TTCCAAC TGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCC 120

Qy 219 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 278  
|||||

Db 121 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 180

Qy 279 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG 338  
|||||

Db 181 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG 240

|    |     |   |     |
|----|-----|---|-----|
| Qy | 339 | GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG  | 398 |
|    |     |   |     |
| Db | 241 | GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG  | 300 |
| Qy | 399 | AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG  | 458 |
|    |     |   |     |
| Db | 301 | AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG  | 360 |
| Qy | 459 | AGCAATGAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT   | 518 |
|    |     |   |     |
| Db | 361 | AGCAATGAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT   | 420 |
| Qy | 519 | CTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT | 578 |
|    |     |   |     |
| Db | 421 | CTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT | 480 |
| Qy | 579 | TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT  | 638 |
|    |     |   |     |
| Db | 481 | TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT  | 540 |
| Qy | 639 | GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG  | 698 |
|    |     |   |     |
| Db | 541 | GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG  | 600 |
| Qy | 699 | AACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC  | 758 |
|    |     |   |     |
| Db | 601 | AACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC  | 660 |
| Qy | 759 | AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT  | 818 |
|    |     |   |     |
| Db | 661 | AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT  | 720 |
| Qy | 819 | TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG  | 878 |
|    |     |   |     |
| Db | 721 | TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG  | 780 |
| Qy | 879 | AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG  | 938 |
|    |     |   |     |
| Db | 781 | AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCG-AAARCTG  | 839 |
| Qy | 939 | CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGC     | 996 |
|    |     | :   |     |
| Db | 840 | CTGCAGAAGAAGTGGACCMCCTCCTGAAGCCCACYGCTCMCCAGCCCGGGCACTGC      | 897 |

# RESULT 12

BX328255

LOCUS BX328255 897 bp mRNA linear EST 07-APR-2004

DEFINITION BX328255 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED

Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.

ACCESSION BX328255

VERSION BX328255.2 GI:46262160

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 897)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 1, 2003 this sequence version replaced gi:30307730.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 907.f  
 For more information about this cluster, see  
[http://www.genoscope.cns.fr/cdna?s=CS0BAG053ZH06\\_CS05040\\_1&c=907.f](http://www.genoscope.cns.fr/cdna?s=CS0BAG053ZH06_CS05040_1&c=907.f).

FEATURES Location/Qualifiers  
 source 1. .897  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DL005YC17"  
 /cell\_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"  
 /cell\_line="RAMOS CELL LINE"  
 /clone\_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT  
 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

# ORIGIN

Query Match 26.7%; Score 839; DB 5; Length 897;  
 Best Local Similarity 99.0%; Pred. No. 1.5e-210;  
 Matches 886; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

|    |      |  |      |
|----|------|--|------|
| Qy | 805  | TGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGG-AGACAGCCAGCGAG | 863  |
|    |      |  |      |
| Db | 1    | TGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAAGACAGCCAGCGAG | 60   |
| Qy | 864  | TTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTG | 923  |
|    |      |  |      |
| Db | 61   | TTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTG | 120  |
| Qy | 924  | GGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGC  | 983  |
|    |      |  |      |
| Db | 121  | GGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGC  | 180  |
| Qy | 984  | ACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGAT  | 1043 |
|    |      |  |      |
| Db | 181  | ACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGAT  | 240  |
| Qy | 1044 | TCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGACC   | 1103 |
|    |      |  |      |
| Db | 241  | TCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGACC   | 300  |

|    |      |   |      |
|----|------|---|------|
| Qy | 1104 | AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA  | 1163 |
|    |      |   |      |
| Db | 301  | AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA  | 360  |
| Qy | 1164 | TACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAAC  | 1223 |
|    |      |   |      |
| Db | 361  | TACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAAC  | 420  |
| Qy | 1224 | CCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG | 1283 |
|    |      |   |      |
| Db | 421  | CCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG | 480  |
| Qy | 1284 | GACCATTTCTTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTG | 1343 |
|    |      |   |      |
| Db | 481  | GACCATTTCTTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTG | 540  |
| Qy | 1344 | GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC  | 1403 |
|    |      |   |      |
| Db | 541  | GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC  | 600  |
| Qy | 1404 | ATGTACCTGGGAACCAACACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT  | 1463 |
|    |      |   |      |
| Db | 601  | ATGTACCTGGGAACCAACACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT  | 660  |
| Qy | 1464 | GCTCATCTGGTGAAGAGATTTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAG | 1523 |
|    |      |   |      |
| Db | 661  | GCTCATCTGGTGAAGAGATTTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAG | 720  |
| Qy | 1524 | CTGGCCCCCACCAGGGTGCA-GTGTGGTAGGCTTCTCAGGAGGTGTCTGG-AGGGTGC    | 1581 |
|    |      |   |      |
| Db | 721  | CTGGCCCCCACCAGGGTGCA-GTGTGGTAGGCTTCTCAGGAGGTGTCTGGNAGGGTGC    | 780  |
| Qy | 1582 | CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGACCCCC  | 1641 |
|    |      |   |      |
| Db | 781  | CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGACCCCC  | 840  |
| Qy | 1642 | ACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCT       | 1696 |
|    |      |   |      |
| Db | 841  | -CTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCT       | 894  |

# RESULT 13

BQ057192

LOCUS BQ057192 974 bp mRNA linear EST 29-MAR-2002

DEFINITION AGENCOURT\_6769628 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5812383 5', mRNA sequence.

ACCESSION BQ057192

VERSION BQ057192.1 GI:19816532

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 974)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)



JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Lou Staudt  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2062 row: 1 column: 16  
High quality sequence stop: 714.

FEATURES Location/Qualifiers  
source 1. .974  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5812383"  
/tissue\_type="lymphoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_99"  
/note="Organ: lymph; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCACGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

# ORIGIN

Query Match 26.3%; Score 827.4; DB 5; Length 974;  
Best Local Similarity 92.6%; Pred. No. 1.8e-207;  
Matches 902; Conservative 0; Mismatches 67; Indels 5; Gaps 3;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 92  | TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCCT | 151 |
|    |     |   |     |
| Db | 1   | TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCCT | 60  |
| Qy | 152 | TTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCA | 211 |
|    |     |   |     |
| Db | 61  | TTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCA | 120 |
| Qy | 212 | GGGGCCCATGCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT   | 271 |
|    |     |   |     |
| Db | 121 | GGGGCCCATGCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT   | 180 |
| Qy | 272 | CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT  | 331 |
|    |     |   |     |
| Db | 181 | CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT  | 240 |
| Qy | 332 | CTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG  | 391 |
|    |     |   |     |
| Db | 241 | CTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG  | 300 |
| Qy | 392 | GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAA  | 451 |

```

      |||
Db      301 GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAA 360
Qy      452 GAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGT 511
      |||
Db      361 GAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGT 420
Qy      512 CACCCATCTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCTTCATTGAACT 571
      |||
Db      421 CACCCATCTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCTTCATTGAACT 480
Qy      572 TCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG 631
      |||
Db      481 TCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG 540
Qy      632 CCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGG 691
      |||
Db      541 CCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGG 600
Qy      692 TACTATGAACAACTTCCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCCAGCC 751
      |||
Db      601 TACTATGAACAACTTCCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCCAGCC 660
Qy      752 TGTCCCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC 811
      |||
Db      661 TGTCCCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC 720
Qy      812 CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTT 871
      |||
Db      721 CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTT 780
Qy      872 CTTTGAGAGGCTCCACACATCGCGGGTGG-CTAGAGTCTGCAAGAATGACGTGGGC-GGC 929
      |||
Db      781 CTTTGAGAGGCCCCACCCTCCCGGGGGGCTANAGTCTGCCAAAATGACGTGGGCGGGC 840
Qy      930 GAAAAGCTGCTGCAGAAGAA---GTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACC 986
      |||
Db      841 GAAAAGCTGCTGCAAAAAAAGTGGACCCCTTCCTTGAAGGCCAGCTGCTCTGGCCC 900
Qy      987 CAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCT 1046
      | | | | |
Db      901 CCAGCCGGGGGAGCTTGCCCTTTCACGTCATTCCCGCCCCGGGGTCTGGCTCCCCC 960
Qy      1047 CCCACAGCTCCCCA 1060
      || |
Db      961 CCGAATTTTCCCCA 974

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RESULT 14

BX390196

LOCUS BX390196 944 bp mRNA linear EST 29-APR-2004

DEFINITION BX390196 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens  
cDNA clone CS0DD003YE08 5-PRIME, mRNA sequence.

ACCESSION BX390196

VERSION BX390196.2 GI:46873199

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 944)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30463276.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 907.f  
 For more information about this cluster, see  
[http://www.genoscope.cns.fr/cdna?s=CS0BAG009ZD12\\_CS00860\\_1&c=907.f](http://www.genoscope.cns.fr/cdna?s=CS0BAG009ZD12_CS00860_1&c=907.f).

FEATURES Location/Qualifiers

source 1. .944  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DD003YE08"  
 /tissue\_type="NEUROBLASTOMA COT 50-NORMALIZED"  
 /clone\_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

# ORIGIN

Query Match 26.1%; Score 820.4; DB 5; Length 944;  
 Best Local Similarity 97.4%; Pred. No. 1.3e-205;  
 Matches 897; Conservative 0; Mismatches 17; Indels 7; Gaps 6;

|    |      |  |      |
|----|------|--|------|
| Qy | 1535 | CCAGGGTGCACTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTG | 1594 |
|    |      |  |      |
| Db | 1    | CCAGGGTGCACTGTTTGTAGGCTTCT-AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTG | 59   |
| Qy | 1595 | TAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGA | 1654 |
|    |      |  |      |
| Db | 60   | TAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGA | 119  |
| Qy | 1655 | CCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGA  | 1714 |
|    |      |  |      |
| Db | 120  | CCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGA  | 179  |
| Qy | 1715 | CATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCG  | 1774 |
|    |      |  |      |
| Db | 180  | CATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCG  | 239  |
| Qy | 1775 | GCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGA  | 1834 |
|    |      |  |      |
| Db | 240  | GCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGA  | 299  |

|    |      |   |      |
|----|------|---|------|
| Qy | 1835 | GCTCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGC    | 1894 |
|    |      |   |      |
| Db | 300  | GCTCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGC    | 359  |
| Qy | 1895 | AGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGG  | 1954 |
|    |      |   |      |
| Db | 360  | AGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGG  | 419  |
| Qy | 1955 | AGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTC  | 2014 |
|    |      |   |      |
| Db | 420  | AGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTC  | 479  |
| Qy | 2015 | CTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAGTGGCAGGCATCCC  | 2074 |
|    |      |   |      |
| Db | 480  | CTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAGTGGCAGGCATCCC  | 539  |
| Qy | 2075 | CCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCA  | 2134 |
|    |      |   |      |
| Db | 540  | CCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCA  | 599  |
| Qy | 2135 | GCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCCTCTTGCCTTAGTGCTTTCAGG  | 2194 |
|    |      |   |      |
| Db | 600  | GCAGTCCTACTGGCCCCACTTGTCACTGTCACTGTCCCTCTTGCCTTAGTGCTTTCAGG   | 659  |
| Qy | 2195 | AGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTC- | 2253 |
|    |      |   |      |
| Db | 660  | AGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTTCGGGCAAGGTTCA  | 719  |
| Qy | 2254 | AGGGCTGTGAGACCCTGCGCCCTGGGG--AGAAGGCCCGTTAAGCAGAGAGCAACA-CC   | 2310 |
|    |      |   |      |
| Db | 720  | AGGGCTGTGAGACCCTGCGCCCTGGGGGAGAAAGGCCCGTTAAGCAGAGAGCAACACCC   | 779  |
| Qy | 2311 | TCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACG-CTGACAACAACCTGC | 2369 |
|    |      |   |      |
| Db | 780  | TTCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGGCGCCTGACAACAACCTGC | 839  |
| Qy | 2370 | CTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGG  | 2429 |
|    |      |   |      |
| Db | 840  | CTAGGCACTGAGGTAGCTTAAACTCTA-GCACAGCCGGGGCTTGCGGGGCAGCCACCTGC  | 898  |
| Qy | 2430 | CCATGCTGGCTGGGCGGCCCA   | 2450 |
|    |      |   |      |
| Db | 899  | CCATGCTGTGTGGGCGGCCCA   | 919  |

RESULT 15  
CB243787/c

|            |  |        |      |        |                 |
|------------|--|--------|------|--------|-----------------|
| LOCUS      | CB243787   | 797 bp | mRNA | linear | EST 12-FEB-2003 |
| DEFINITION | UI-CF-FN0-agg-a-05-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone<br>UI-CF-FN0-agg-a-05-0-UI 3', mRNA sequence. |        |      |        |                 |
| ACCESSION  | CB243787   |        |      |        |                 |
| VERSION    | CB243787.1 GI:28365431   |        |      |        |                 |
| KEYWORDS   | EST.   |        |      |        |                 |
| SOURCE     | Homo sapiens (human)   |        |      |        |                 |
| ORGANISM   | Homo sapiens<br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                          |        |      |        |                 |

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 797)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
 The following repetitive elements were found in this cDNA sequence: 1-46, >AT rich#Low\_complexity (matched compliment)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES

source Location/Qualifiers

1. .797

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-CF-FN0-agg-a-05-0-UI"

/tissue\_type="Human Lung Epithelial cells"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-CF-FN0"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-CF-FN0 is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu

TAG\_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h

TAG\_LIB=UI-CF-FN0

TAG\_SEQ=CTGCTCAGGT"

#### ORIGIN

Query Match 24.8%; Score 779.8; DB 6; Length 797;

Best Local Similarity 99.4%; Pred. No. 7e-195;

Matches 781; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2358 GACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT 2417

|||||

Db 797 GACAACAACCTGCNTAGGCACTGAGGTAGCTTAAACTNTAGGCACAGGCCGGGGCTGCGGT 738

|    |      |  |      |
|----|------|--|------|
| Qy | 2418 | GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA   | 2477 |
|    |      |  |      |
| Db | 737  | GCAGGCACCCGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGANTAGGATGACAGCA   | 678  |
| Qy | 2478 | GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC   | 2537 |
|    |      |  |      |
| Db | 677  | GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC   | 618  |
| Qy | 2538 | ACTCAGCAGGGTGATGCACAGCAGTCTGCCCTCCCCTATGGGACTCCCTTCTACCAAGCAC  | 2597 |
|    |      |  |      |
| Db | 617  | ACTCAGCAGGGTGATGCACAGCAGTCTGCCCTCCCCTATGGGACTCCCTTCTACCAAGCAC  | 558  |
| Qy | 2598 | ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA   | 2657 |
|    |      |  |      |
| Db | 557  | ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA   | 498  |
| Qy | 2658 | ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTC  | 2717 |
|    |      |  |      |
| Db | 497  | ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTC  | 438  |
| Qy | 2718 | AAGAGACCCATAAAAAACCTGCCTGTCCCAGGACCCCTATGGTAATGAACACCAAACATCTA | 2777 |
|    |      |  |      |
| Db | 437  | AAGAGACCCATAAAAAACCTGCCTGTCCTAGGACCCCTATGGTAATGAACACCAAACATCTA | 378  |
| Qy | 2778 | AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC   | 2837 |
|    |      |  |      |
| Db | 377  | AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC   | 318  |
| Qy | 2838 | ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA   | 2897 |
|    |      |  |      |
| Db | 317  | ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA   | 258  |
| Qy | 2898 | GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCT    | 2957 |
|    |      |  |      |
| Db | 257  | GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCT    | 198  |
| Qy | 2958 | TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCC   | 3017 |
|    |      |  |      |
| Db | 197  | TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCC   | 138  |
| Qy | 3018 | TTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCCTTTGTTT  | 3077 |
|    |      |  |      |
| Db | 137  | TTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCCTTTGTTT  | 78   |
| Qy | 3078 | TGGGATTTCAGAAAACCTGCTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTA | 3137 |
|    |      |  |      |
| Db | 77   | TGGGATTTCAGAAAACCTGCTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTA | 18   |
| Qy | 3138 | AAAAAA 3143  |      |
|    |      |  |      |
| Db | 17   | AAAAAA 12  |      |

Search completed: February 15, 2005, 13:17:35  
Job time : 9877 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 22:56:12 ; Search time 9798 Seconds  
(without alignments)  
12210.247 Million cell updates/sec

Title: US-10-015-391A-276  
Perfect score: 3143  
Sequence: 1 gggctgaggcactgagagac.....aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result<br>No. | Score  | Query |        | DB | ID        | Description        |
|---------------|--------|-------|--------|----|-----------|--------------------|
|               |        | Match | Length |    |           |                    |
| 1             | 3005   | 95.6  | 3005   | 3  | CR623694  | CR623694 full-leng |
| 2             | 2927.6 | 93.1  | 3151   | 3  | HSM807023 | BX640891 Homo sapi |
| 3             | 1874   | 59.6  | 2172   | 9  | AY402621  | AY402621 Homo sapi |
| 4             | 1765.4 | 56.2  | 2133   | 9  | AY402622  | AY402622 Pan trogl |
| 5             | 1747.4 | 55.6  | 3206   | 3  | AK077976  | AK077976 Mus muscu |
| 6             | 1701.4 | 54.1  | 3086   | 3  | AK035918  | AK035918 Mus muscu |
| 7             | 1372.2 | 43.7  | 2172   | 9  | AY402623  | AY402623 Mus muscu |
| c 8           | 950.6  | 30.2  | 1108   | 5  | BX367242  | BX367242 BX367242  |

|   |    |       |      |      |   |          |          |           |
|---|----|-------|------|------|---|----------|----------|-----------|
| c | 9  | 926.2 | 29.5 | 1064 | 5 | BX363741 | BX363741 | BX363741  |
| c | 10 | 874.4 | 27.8 | 922  | 5 | BX350606 | BX350606 | BX350606  |
|   | 11 | 849.2 | 27.0 | 934  | 5 | BX384966 | BX384966 | BX384966  |
|   | 12 | 839   | 26.7 | 897  | 5 | BX328255 | BX328255 | BX328255  |
|   | 13 | 827.4 | 26.3 | 974  | 5 | BQ057192 | BQ057192 | AGENCOURT |
|   | 14 | 820.4 | 26.1 | 944  | 5 | BX390196 | BX390196 | BX390196  |
| c | 15 | 779.8 | 24.8 | 797  | 6 | CB243787 | CB243787 | UI-CF-FN0 |
|   | 16 | 775   | 24.7 | 801  | 5 | BX112994 | BX112994 | BX112994  |
|   | 17 | 769.8 | 24.5 | 912  | 5 | BQ883972 | BQ883972 | AGENCOURT |
|   | 18 | 768   | 24.4 | 958  | 5 | BX376660 | BX376660 | BX376660  |
|   | 19 | 757.6 | 24.1 | 892  | 6 | CD107028 | CD107028 | AGENCOURT |
| c | 20 | 756.2 | 24.1 | 819  | 6 | CD631371 | CD631371 | 56050427H |
|   | 21 | 748.6 | 23.8 | 951  | 5 | BQ056228 | BQ056228 | AGENCOURT |
|   | 22 | 696.6 | 22.2 | 775  | 1 | AU122156 | AU122156 | AU122156  |
|   | 23 | 691.2 | 22.0 | 970  | 5 | BQ707628 | BQ707628 | AGENCOURT |
|   | 24 | 681   | 21.7 | 1066 | 4 | BM806752 | BM806752 | AGENCOURT |
| c | 25 | 675.2 | 21.5 | 763  | 6 | CD631373 | CD631373 | 56066030H |
|   | 26 | 674   | 21.4 | 727  | 7 | CN255817 | CN255817 | 170004252 |
|   | 27 | 673   | 21.4 | 960  | 5 | BX367243 | BX367243 | BX367243  |
|   | 28 | 666   | 21.2 | 706  | 6 | CD631372 | CD631372 | 56050427J |
|   | 29 | 664   | 21.1 | 681  | 7 | CV023527 | CV023527 | 490 Full  |
|   | 30 | 661.8 | 21.1 | 666  | 4 | BG684636 | BG684636 | 602635914 |
|   | 31 | 650   | 20.7 | 925  | 5 | BQ937439 | BQ937439 | AGENCOURT |
| c | 32 | 627.4 | 20.0 | 640  | 6 | CA311774 | CA311774 | UI-CF-FN0 |
| c | 33 | 612   | 19.5 | 624  | 4 | BM666780 | BM666780 | UI-E-CL1- |
|   | 34 | 609.8 | 19.4 | 1119 | 4 | BI550650 | BI550650 | 603195823 |
|   | 35 | 608.4 | 19.4 | 803  | 7 | CN539797 | CN539797 | UI-M-HU0- |
|   | 36 | 598.6 | 19.0 | 621  | 2 | AW965845 | AW965845 | EST377918 |
| c | 37 | 598.4 | 19.0 | 634  | 5 | BU632880 | BU632880 | UI-H-FE1- |
| c | 38 | 594   | 18.9 | 618  | 5 | BU686374 | BU686374 | UI-CF-DU1 |
|   | 39 | 590.8 | 18.8 | 740  | 6 | CD631374 | CD631374 | 56066030J |
|   | 40 | 585.2 | 18.6 | 881  | 5 | BQ960065 | BQ960065 | AGENCOURT |
|   | 41 | 579.2 | 18.4 | 720  | 6 | CA315771 | CA315771 | UI-M-FW0- |
|   | 42 | 579   | 18.4 | 580  | 5 | BP346261 | BP346261 | BP346261  |
|   | 43 | 576.2 | 18.3 | 582  | 5 | BP312448 | BP312448 | BP312448  |
|   | 44 | 568.6 | 18.1 | 783  | 7 | CK483764 | CK483764 | AGENCOURT |
|   | 45 | 566.8 | 18.0 | 582  | 5 | BP305311 | BP305311 | BP305311  |
|   | 46 | 565.8 | 18.0 | 571  | 7 | CR554650 | CR554650 | DKFZp4590 |
|   | 47 | 557.8 | 17.7 | 796  | 5 | BU052878 | BU052878 | UI-M-FC0- |
|   | 48 | 554.4 | 17.6 | 718  | 7 | CK837783 | CK837783 | 4063044 B |
|   | 49 | 552.6 | 17.6 | 917  | 6 | CA454892 | CA454892 | AGENCOURT |
|   | 50 | 552.4 | 17.6 | 779  | 4 | BI683727 | BI683727 | 603306287 |
|   | 51 | 551.4 | 17.5 | 695  | 4 | BG685741 | BG685741 | 602637838 |
|   | 52 | 547   | 17.4 | 547  | 4 | BM128651 | BM128651 | if14b09.y |
|   | 53 | 546.6 | 17.4 | 709  | 5 | BQ573544 | BQ573544 | UI-M-FD0- |
|   | 54 | 542.6 | 17.3 | 667  | 4 | BG703963 | BG703963 | 602687061 |
|   | 55 | 542.2 | 17.3 | 784  | 5 | BQ043061 | BQ043061 | UI-M-EG0p |
|   | 56 | 538.6 | 17.1 | 841  | 6 | CB566426 | CB566426 | AGENCOURT |
|   | 57 | 530   | 16.9 | 550  | 5 | BP292524 | BP292524 | BP292524  |
|   | 58 | 528   | 16.8 | 528  | 6 | CA393520 | CA393520 | cs39b03.y |
|   | 59 | 526.2 | 16.7 | 944  | 4 | BI250501 | BI250501 | 602993551 |
|   | 60 | 524.4 | 16.7 | 858  | 7 | CK022938 | CK022938 | AGENCOURT |
| c | 61 | 522.4 | 16.6 | 536  | 5 | BQ356019 | BQ356019 | PM3-HT130 |
|   | 62 | 510.8 | 16.3 | 793  | 4 | BI146386 | BI146386 | 602910749 |
|   | 63 | 510   | 16.2 | 666  | 2 | BE868099 | BE868099 | 601443414 |
|   | 64 | 507.8 | 16.2 | 519  | 7 | CK819350 | CK819350 | if14b09.y |
|   | 65 | 500.2 | 15.9 | 532  | 4 | BM691378 | BM691378 | UI-E-CI1- |



|   |     |       |      |     |   |          |          |             |
|---|-----|-------|------|-----|---|----------|----------|-------------|
|   | 66  | 500.2 | 15.9 | 758 | 4 | BI105301 | BI105301 | 602893591   |
| c | 67  | 498   | 15.8 | 567 | 1 | AU147813 | AU147813 | AU147813    |
|   | 68  | 495.4 | 15.8 | 628 | 7 | CN792080 | CN792080 | 4126901 B   |
|   | 69  | 494   | 15.7 | 598 | 2 | BE588408 | BE588408 | 194035 BA   |
|   | 70  | 486.6 | 15.5 | 788 | 7 | CK481778 | CK481778 | AGENCOURT   |
|   | 71  | 486   | 15.5 | 969 | 4 | BG247839 | BG247839 | 602359548   |
|   | 72  | 481.6 | 15.3 | 632 | 7 | CK625364 | CK625364 | mi32c08.y   |
|   | 73  | 481   | 15.3 | 481 | 4 | BM694992 | BM694992 | UI-E-CL1-   |
| c | 74  | 478.8 | 15.2 | 503 | 1 | AI817099 | AI817099 | wj76h11.x   |
|   | 75  | 478.8 | 15.2 | 810 | 6 | CB587284 | CB587284 | AGENCOURT   |
|   | 76  | 476.8 | 15.2 | 544 | 4 | BI481387 | BI481387 | H2RPE-174   |
|   | 77  | 470.4 | 15.0 | 530 | 1 | AA481246 | AA481246 | aa34h11.r   |
| c | 78  | 469.2 | 14.9 | 562 | 2 | AW836429 | AW836429 | PM3-LT003   |
|   | 79  | 467.8 | 14.9 | 821 | 5 | BQ442696 | BQ442696 | UI-M-EV0-   |
|   | 80  | 465.4 | 14.8 | 806 | 7 | CK481746 | CK481746 | AGENCOURT   |
|   | 81  | 464.6 | 14.8 | 585 | 4 | BI359871 | BI359871 | 384615 MA   |
|   | 82  | 462.6 | 14.7 | 667 | 2 | AW914963 | AW914963 | EST346267   |
|   | 83  | 462.2 | 14.7 | 887 | 4 | BI219079 | BI219079 | 602938695   |
|   | 84  | 461.4 | 14.7 | 672 | 6 | BY747595 | BY747595 | BY747595    |
|   | 85  | 461.2 | 14.7 | 892 | 5 | BQ934892 | BQ934892 | AGENCOURT   |
|   | 86  | 449.6 | 14.3 | 537 | 2 | AW657913 | AW657913 | 93554 MAR   |
|   | 87  | 447   | 14.2 | 872 | 4 | BI150290 | BI150290 | 602915311   |
| c | 88  | 446.4 | 14.2 | 450 | 1 | AI568200 | AI568200 | tn66h01.x   |
|   | 89  | 444   | 14.1 | 822 | 7 | CO565372 | CO565372 | AGENCOURT   |
|   | 90  | 443.8 | 14.1 | 659 | 6 | BY747925 | BY747925 | BY747925    |
| c | 91  | 443.4 | 14.1 | 456 | 5 | BU726485 | BU726485 | UI-E-CI1-   |
| c | 92  | 442.4 | 14.1 | 444 | 5 | BQ356020 | BQ356020 | PM3-HT130   |
| c | 93  | 440.6 | 14.0 | 468 | 5 | BQ356018 | BQ356018 | PM3-HT130   |
|   | 94  | 439.6 | 14.0 | 578 | 4 | BI341318 | BI341318 | 368709 MA   |
| c | 95  | 436.8 | 13.9 | 440 | 1 | AA973640 | AA973640 | oo48c04.s   |
|   | 96  | 435.2 | 13.8 | 579 | 4 | BI360284 | BI360284 | 387146 MA   |
|   | 97  | 432.4 | 13.8 | 621 | 9 | CG591258 | CG591258 | OST245642   |
|   | 98  | 431   | 13.7 | 632 | 7 | CO581119 | CO581119 | ILLUMIGEN   |
|   | 99  | 430.8 | 13.7 | 794 | 2 | BF578994 | BF578994 | 602096109   |
|   | 100 | 427   | 13.6 | 563 | 4 | BM030859 | BM030859 | 495387 MA   |
| c | 101 | 426.8 | 13.6 | 441 | 1 | AA554541 | AA554541 | nl14b01.s   |
|   | 102 | 426.8 | 13.6 | 827 | 7 | CO404310 | CO404310 | AGENCOURT   |
|   | 103 | 425.2 | 13.5 | 443 | 2 | BF882612 | BF882612 | QV3-ET020   |
| c | 104 | 425.2 | 13.5 | 457 | 1 | AI291110 | AI291110 | qml0d09.x   |
|   | 105 | 422.8 | 13.5 | 546 | 2 | BF199358 | BF199358 | 249500 MA   |
|   | 106 | 422.4 | 13.4 | 759 | 4 | BG243769 | BG243769 | 602357081   |
|   | 107 | 418.4 | 13.3 | 576 | 4 | BI345630 | BI345630 | 374508 MA   |
| c | 108 | 415   | 13.2 | 415 | 1 | AI017230 | AI017230 | ou32d12.x   |
|   | 109 | 415   | 13.2 | 536 | 2 | BF199378 | BF199378 | 249524 MA   |
| c | 110 | 414.6 | 13.2 | 454 | 2 | BF882611 | BF882611 | QV3-ET020   |
|   | 111 | 414.6 | 13.2 | 538 | 2 | BF080018 | BF080018 | 230753 MA   |
| c | 112 | 413.6 | 13.2 | 537 | 5 | BX372943 | BX372943 | BX372943    |
|   | 113 | 413   | 13.1 | 583 | 5 | BP315573 | BP315573 | BP315573    |
| c | 114 | 412.6 | 13.1 | 468 | 7 | T34379   | T34379   | EST66750 Hu |
|   | 115 | 412   | 13.1 | 582 | 5 | BP314196 | BP314196 | BP314196    |
|   | 116 | 411   | 13.1 | 581 | 5 | BP314893 | BP314893 | BP314893    |
|   | 117 | 410.8 | 13.1 | 624 | 4 | BM691301 | BM691301 | UI-E-CI1-   |
|   | 118 | 409   | 13.0 | 582 | 5 | BP312657 | BP312657 | BP312657    |
|   | 119 | 409   | 13.0 | 721 | 2 | BF580373 | BF580373 | 602097124   |
|   | 120 | 408   | 13.0 | 473 | 7 | H08023   | H08023   | yl91d06.r1  |
|   | 121 | 406   | 12.9 | 406 | 7 | CR538178 | CR538178 | DKFZp459F   |
|   | 122 | 405   | 12.9 | 583 | 5 | BP314892 | BP314892 | BP314892    |

|   |     |       |      |      |   |          |          |             |
|---|-----|-------|------|------|---|----------|----------|-------------|
|   | 123 | 404.8 | 12.9 | 870  | 2 | BE306403 | BE306403 | 601102295   |
|   | 124 | 404.6 | 12.9 | 610  | 4 | BG618720 | BG618720 | 602645175   |
|   | 125 | 403.2 | 12.8 | 1122 | 2 | BF159534 | BF159534 | 601769029   |
| c | 126 | 402.6 | 12.8 | 449  | 1 | AI623385 | AI623385 | ts18g03.x   |
|   | 127 | 401.4 | 12.8 | 581  | 5 | BP357544 | BP357544 | BP357544    |
|   | 128 | 395.4 | 12.6 | 634  | 1 | AA646591 | AA646591 | ve46d08.r   |
|   | 129 | 394.8 | 12.6 | 494  | 4 | BM288077 | BM288077 | 528964 MA   |
|   | 130 | 392.4 | 12.5 | 766  | 7 | CK478839 | CK478839 | AGENCOURT   |
|   | 131 | 392.2 | 12.5 | 882  | 2 | BE571537 | BE571537 | 601333983   |
|   | 132 | 392   | 12.5 | 582  | 5 | BP315572 | BP315572 | BP315572    |
|   | 133 | 391.6 | 12.5 | 555  | 6 | CB613565 | CB613565 | AMGNNUC:N   |
|   | 134 | 390.6 | 12.4 | 581  | 6 | CB606887 | CB606887 | AMGNNUC:N   |
|   | 135 | 388.8 | 12.4 | 465  | 2 | BF882607 | BF882607 | QV3-ET020   |
|   | 136 | 388   | 12.3 | 618  | 6 | CB579294 | CB579294 | AMGNNUC:N   |
|   | 137 | 387.4 | 12.3 | 544  | 4 | BI961174 | BI961174 | MONO1_7_A   |
| c | 138 | 387   | 12.3 | 405  | 1 | AI221749 | AI221749 | qg93f04.x   |
|   | 139 | 383   | 12.2 | 713  | 6 | BY763638 | BY763638 | BY763638    |
| c | 140 | 380.8 | 12.1 | 412  | 1 | AA761091 | AA761091 | ny13g11.s   |
|   | 141 | 378   | 12.0 | 598  | 1 | AV617761 | AV617761 | AV617761    |
|   | 142 | 377.4 | 12.0 | 535  | 5 | BQ552175 | BQ552175 | H4013H07-   |
|   | 143 | 377.2 | 12.0 | 665  | 4 | BI151295 | BI151295 | 602917272   |
| c | 144 | 374.4 | 11.9 | 459  | 2 | BF154829 | BF154829 | PM2-BT076   |
| c | 145 | 374.4 | 11.9 | 459  | 4 | BG949399 | BG949399 | PM2-BT076   |
|   | 146 | 372.4 | 11.8 | 582  | 5 | BP314933 | BP314933 | BP314933    |
|   | 147 | 370.6 | 11.8 | 600  | 6 | CA530364 | CA530364 | 9034-81 M   |
|   | 148 | 370.2 | 11.8 | 541  | 2 | AW654459 | AW654459 | 103930 MA   |
| c | 149 | 369.4 | 11.8 | 464  | 5 | BQ356179 | BQ356179 | PM3-HT130   |
|   | 150 | 367.4 | 11.7 | 490  | 2 | AW659681 | AW659681 | 97213 MAR   |
|   | 151 | 367   | 11.7 | 516  | 2 | BF075002 | BF075002 | 223731 MA   |
| c | 152 | 366.4 | 11.7 | 369  | 2 | AW593031 | AW593031 | hg07e10.x   |
|   | 153 | 363.8 | 11.6 | 368  | 1 | AA419534 | AA419534 | zv03c09.r   |
|   | 154 | 363.4 | 11.6 | 513  | 4 | BM106299 | BM106299 | 509997 MA   |
|   | 155 | 360.6 | 11.5 | 742  | 6 | CB249229 | CB249229 | UI-M-FC0-   |
|   | 156 | 356.4 | 11.3 | 583  | 5 | BP357148 | BP357148 | BP357148    |
|   | 157 | 355   | 11.3 | 529  | 5 | BU698229 | BU698229 | LL2in1365   |
| c | 158 | 354.4 | 11.3 | 363  | 1 | AI221756 | AI221756 | qg93f12.x   |
|   | 159 | 353   | 11.2 | 576  | 4 | BI914790 | BI914790 | 603184176   |
| c | 160 | 351.4 | 11.2 | 737  | 7 | CO425778 | CO425778 | UI-M-HU0-   |
|   | 161 | 348   | 11.1 | 360  | 7 | T19441   | T19441   | f03002s Tes |
| c | 162 | 346   | 11.0 | 358  | 1 | AI682007 | AI682007 | tp45g08.x   |
|   | 163 | 344.8 | 11.0 | 502  | 5 | BU696522 | BU696522 | LL2in1072   |
|   | 164 | 344.2 | 11.0 | 623  | 2 | BB628588 | BB628588 | BB628588    |
|   | 165 | 343.6 | 10.9 | 424  | 2 | AW352877 | AW352877 | 35717 MAR   |
|   | 166 | 340.4 | 10.8 | 552  | 2 | AW655294 | AW655294 | 106095 MA   |
|   | 167 | 338.6 | 10.8 | 449  | 5 | BQ336149 | BQ336149 | PM0-MT042   |
|   | 168 | 337.2 | 10.7 | 545  | 2 | AW654538 | AW654538 | 104068 MA   |
|   | 169 | 334.8 | 10.7 | 479  | 4 | BM088355 | BM088355 | 501805 MA   |
|   | 170 | 333.2 | 10.6 | 411  | 2 | BE859656 | BE859656 | UI-M-AL0-   |
|   | 171 | 332.2 | 10.6 | 443  | 2 | AW355069 | AW355069 | 37338 MAR   |
|   | 172 | 327.4 | 10.4 | 700  | 5 | BM944176 | BM944176 | UI-M-EH0p   |
| c | 173 | 326.8 | 10.4 | 330  | 7 | CK819349 | CK819349 | if14b09.x   |
|   | 174 | 321.8 | 10.2 | 469  | 1 | AJ650325 | AJ650325 | AJ650325    |
|   | 175 | 321.2 | 10.2 | 445  | 2 | AW481698 | AW481698 | 37332 MAR   |
|   | 176 | 320.6 | 10.2 | 433  | 2 | AW355070 | AW355070 | 37337 MAR   |
|   | 177 | 318.6 | 10.1 | 390  | 6 | CB778065 | CB778065 | AMGNNUC:C   |
|   | 178 | 318.4 | 10.1 | 432  | 2 | BF019645 | BF019645 | ux14b02.y   |
| c | 179 | 316.8 | 10.1 | 353  | 2 | AW628784 | AW628784 | hi39e03.x   |

|   |     |       |      |      |   |          |                    |
|---|-----|-------|------|------|---|----------|--------------------|
|   | 180 | 316.2 | 10.1 | 465  | 7 | R81743   | R81743 yj05d01.r1  |
| c | 181 | 315.8 | 10.0 | 469  | 1 | AI141990 | AI141990 oo17g10.x |
|   | 182 | 312.4 | 9.9  | 443  | 4 | BM106612 | BM106612 510531 MA |
| c | 183 | 310.6 | 9.9  | 346  | 5 | BQ335891 | BQ335891 PM3-MT020 |
| c | 184 | 310   | 9.9  | 356  | 2 | AW298440 | AW298440 UI-H-BW0- |
| c | 185 | 308.4 | 9.8  | 310  | 1 | AA687813 | AA687813 nv12e08.s |
| c | 186 | 308   | 9.8  | 456  | 7 | CV374906 | CV374906 PM3-HT130 |
|   | 187 | 302.6 | 9.6  | 514  | 1 | AA959087 | AA959087 ua08f08.r |
|   | 188 | 302   | 9.6  | 388  | 6 | CB779567 | CB779567 AMGNNUC:N |
|   | 189 | 301   | 9.6  | 582  | 5 | BP250593 | BP250593 BP250593  |
|   | 190 | 299.8 | 9.5  | 717  | 5 | BM946956 | BM946956 UI-M-EH0p |
|   | 191 | 298.6 | 9.5  | 583  | 5 | BU694619 | BU694619 LL2in1402 |
|   | 192 | 298.4 | 9.5  | 437  | 2 | BF605420 | BF605420 271789 MA |
|   | 193 | 293.6 | 9.3  | 435  | 6 | BY596404 | BY596404 BY596404  |
|   | 194 | 293.6 | 9.3  | 480  | 6 | CB537061 | CB537061 772134 MA |
|   | 195 | 293.6 | 9.3  | 512  | 1 | AA510439 | AA510439 vg32e04.r |
| c | 196 | 293.2 | 9.3  | 303  | 7 | T19440   | T19440 f03002t Tes |
|   | 197 | 293   | 9.3  | 439  | 4 | BM030747 | BM030747 495245 MA |
|   | 198 | 289.6 | 9.2  | 689  | 1 | AA274712 | AA274712 vc15g11.r |
|   | 199 | 288.8 | 9.2  | 318  | 2 | BE182018 | BE182018 CM1-HT064 |
|   | 200 | 288.2 | 9.2  | 368  | 2 | AW632286 | AW632286 92080 MAR |
|   | 201 | 287.6 | 9.2  | 655  | 2 | BB621440 | BB621440 BB621440  |
|   | 202 | 287.2 | 9.1  | 475  | 4 | BM286849 | BM286849 527060 MA |
|   | 203 | 286.6 | 9.1  | 418  | 6 | CB765926 | CB765926 AMGNNUC:N |
| c | 204 | 286.4 | 9.1  | 298  | 4 | BM662404 | BM662404 UI-E-CI1- |
|   | 205 | 285.8 | 9.1  | 481  | 7 | W13797   | W13797 ma94g12.r1  |
|   | 206 | 285.8 | 9.1  | 514  | 9 | CG646708 | CG646708 OST393408 |
|   | 207 | 285.6 | 9.1  | 354  | 2 | BE155671 | BE155671 PM2-HT035 |
|   | 208 | 284.4 | 9.0  | 286  | 7 | CN255816 | CN255816 170005325 |
|   | 209 | 283.6 | 9.0  | 398  | 2 | BE014053 | BE014053 125627 MA |
|   | 210 | 280.6 | 8.9  | 532  | 1 | AA575453 | AA575453 vl90b06.r |
|   | 211 | 279.4 | 8.9  | 285  | 7 | CR736197 | CR736197 CR736197  |
|   | 212 | 279   | 8.9  | 512  | 2 | BE012711 | BE012711 122368 MA |
| c | 213 | 273.6 | 8.7  | 343  | 7 | R81500   | R81500 yj05d01.s1  |
| c | 214 | 273.4 | 8.7  | 281  | 7 | Z39973   | Z39973 HSC10E102 n |
|   | 215 | 273   | 8.7  | 736  | 2 | BE288736 | BE288736 601093420 |
|   | 216 | 271.4 | 8.6  | 327  | 7 | Z43916   | Z43916 HSC10E101 n |
|   | 217 | 269.4 | 8.6  | 636  | 6 | BY745271 | BY745271 BY745271  |
|   | 218 | 261.6 | 8.3  | 385  | 6 | CB702615 | CB702615 AMGNNUC:S |
|   | 219 | 261.2 | 8.3  | 338  | 1 | AA193482 | AA193482 zr41d02.r |
|   | 220 | 257.4 | 8.2  | 507  | 2 | BE668290 | BE668290 156950 MA |
|   | 221 | 257.2 | 8.2  | 456  | 2 | BB840212 | BB840212 BB840212  |
|   | 222 | 255   | 8.1  | 307  | 7 | T34380   | T34380 EST66751 Hu |
|   | 223 | 253   | 8.0  | 595  | 7 | CN701121 | CN701121 E0445B08- |
|   | 224 | 248.8 | 7.9  | 2480 | 9 | AY407393 | AY407393 Mus muscu |
|   | 225 | 248.6 | 7.9  | 343  | 2 | AW446374 | AW446374 85396 MAR |
|   | 226 | 247.8 | 7.9  | 407  | 5 | BY201059 | BY201059 BY201059  |
|   | 227 | 247.4 | 7.9  | 339  | 7 | CK942886 | CK942886 4066584 B |
|   | 228 | 247.2 | 7.9  | 415  | 5 | BY237094 | BY237094 BY237094  |
|   | 229 | 244   | 7.8  | 731  | 1 | AI116589 | AI116589 ue27f05.y |
| c | 230 | 241.4 | 7.7  | 528  | 1 | AI350408 | AI350408 qt17b12.x |
|   | 231 | 241   | 7.7  | 330  | 2 | AW483617 | AW483617 55275 MAR |
|   | 232 | 240.6 | 7.7  | 3809 | 3 | AK030331 | AK030331 Mus muscu |
|   | 233 | 239   | 7.6  | 2777 | 3 | AK028896 | AK028896 Mus muscu |
|   | 234 | 234.8 | 7.5  | 548  | 5 | BX515711 | BX515711 BX515711  |
|   | 235 | 233.6 | 7.4  | 517  | 2 | BB867776 | BB867776 BB867776  |
|   | 236 | 233.2 | 7.4  | 359  | 5 | BY344631 | BY344631 BY344631  |

|   |     |       |     |      |   |          |          |           |
|---|-----|-------|-----|------|---|----------|----------|-----------|
|   | 237 | 233   | 7.4 | 529  | 1 | AI119178 | AI119178 | ue23g10.y |
| c | 238 | 232.2 | 7.4 | 259  | 1 | AI698802 | AI698802 | wd31b11.x |
|   | 239 | 229.4 | 7.3 | 352  | 5 | BY209243 | BY209243 | BY209243  |
|   | 240 | 229.4 | 7.3 | 353  | 5 | BY194675 | BY194675 | BY194675  |
|   | 241 | 228.2 | 7.3 | 345  | 6 | CB705908 | CB705908 | AMGNNUC:N |
|   | 242 | 227.6 | 7.2 | 2502 | 9 | AY407391 | AY407391 | Homo sapi |
|   | 243 | 226.2 | 7.2 | 359  | 5 | BY192032 | BY192032 | BY192032  |
|   | 244 | 225.8 | 7.2 | 441  | 2 | BB848500 | BB848500 | BB848500  |
|   | 245 | 222.8 | 7.1 | 354  | 5 | BY186467 | BY186467 | BY186467  |
| c | 246 | 222   | 7.1 | 226  | 1 | AA971074 | AA971074 | op70g02.s |
|   | 247 | 220.6 | 7.0 | 399  | 5 | BY258404 | BY258404 | BY258404  |
| c | 248 | 218.4 | 6.9 | 231  | 1 | AA588098 | AA588098 | nm98h03.s |
|   | 249 | 218.4 | 6.9 | 356  | 5 | BY203094 | BY203094 | BY203094  |
| c | 250 | 216.2 | 6.9 | 224  | 1 | AA481169 | AA481169 | aa34h11.s |
|   | 251 | 216.2 | 6.9 | 555  | 7 | CN699228 | CN699228 | E0418E11- |
|   | 252 | 216.2 | 6.9 | 925  | 5 | BQ929233 | BQ929233 | AGENCOURT |
|   | 253 | 215.4 | 6.9 | 787  | 4 | BI665818 | BI665818 | 603289737 |
|   | 254 | 213.4 | 6.8 | 978  | 5 | BQ219389 | BQ219389 | AGENCOURT |
|   | 255 | 213.2 | 6.8 | 766  | 4 | BI330594 | BI330594 | 602981035 |
|   | 256 | 212.8 | 6.8 | 344  | 5 | BY182086 | BY182086 | BY182086  |
|   | 257 | 212.4 | 6.8 | 342  | 5 | BY190812 | BY190812 | BY190812  |
|   | 258 | 212   | 6.7 | 554  | 1 | AL780781 | AL780781 | AL780781  |
|   | 259 | 211   | 6.7 | 3648 | 3 | AK090073 | AK090073 | Mus muscu |
|   | 260 | 210.6 | 6.7 | 360  | 5 | BY203098 | BY203098 | BY203098  |
|   | 261 | 210   | 6.7 | 350  | 9 | CG604636 | CG604636 | OST280536 |
|   | 262 | 202.8 | 6.5 | 906  | 7 | CF548431 | CF548431 | AGENCOURT |
|   | 263 | 201.6 | 6.4 | 361  | 6 | BY780664 | BY780664 | BY780664  |
|   | 264 | 199.4 | 6.3 | 340  | 5 | BY180833 | BY180833 | BY180833  |
|   | 265 | 198   | 6.3 | 904  | 2 | BF134543 | BF134543 | 601784950 |
|   | 266 | 196.8 | 6.3 | 343  | 5 | BY176481 | BY176481 | BY176481  |
|   | 267 | 194.2 | 6.2 | 457  | 5 | BY225325 | BY225325 | BY225325  |
|   | 268 | 192   | 6.1 | 374  | 6 | CB692309 | CB692309 | AMGNNUC:N |
|   | 269 | 191.8 | 6.1 | 398  | 5 | BY284987 | BY284987 | BY284987  |
|   | 270 | 191.6 | 6.1 | 691  | 7 | CF767810 | CF767810 | CES006164 |
|   | 271 | 190.6 | 6.1 | 298  | 2 | BB586510 | BB586510 | BB586510  |
|   | 272 | 190.4 | 6.1 | 380  | 5 | BY265162 | BY265162 | BY265162  |
|   | 273 | 189.8 | 6.0 | 424  | 5 | BY188709 | BY188709 | BY188709  |
|   | 274 | 189   | 6.0 | 386  | 5 | BY231195 | BY231195 | BY231195  |
|   | 275 | 186.6 | 5.9 | 267  | 4 | BM485185 | BM485185 | 539436 MA |
|   | 276 | 185.4 | 5.9 | 2502 | 9 | AY407392 | AY407392 | Pan trogl |
| c | 277 | 184.6 | 5.9 | 588  | 6 | CB469303 | CB469303 | sn05_G02. |
|   | 278 | 181   | 5.8 | 504  | 2 | BE481474 | BE481474 | 166929 BA |
|   | 279 | 179.2 | 5.7 | 838  | 7 | CF374334 | CF374334 | AGENCOURT |
|   | 280 | 176.4 | 5.6 | 416  | 5 | BY183408 | BY183408 | BY183408  |
| c | 281 | 176   | 5.6 | 560  | 6 | CB476226 | CB476226 | jns118_A0 |
|   | 282 | 172.8 | 5.5 | 710  | 6 | CB422627 | CB422627 | 595748 MA |
|   | 283 | 170   | 5.4 | 312  | 5 | BY170795 | BY170795 | BY170795  |
|   | 284 | 169.2 | 5.4 | 782  | 5 | BP684334 | BP684334 | BP684334  |
|   | 285 | 166.8 | 5.3 | 297  | 5 | BY000550 | BY000550 | BY000550  |
|   | 286 | 165.8 | 5.3 | 356  | 5 | BY233307 | BY233307 | BY233307  |
|   | 287 | 163   | 5.2 | 411  | 6 | BY547048 | BY547048 | BY547048  |
|   | 288 | 163   | 5.2 | 437  | 7 | CV312033 | CV312033 | CM0-PT004 |
|   | 289 | 161.4 | 5.1 | 768  | 5 | BM943605 | BM943605 | UI-M-EH0p |
| c | 290 | 160.4 | 5.1 | 299  | 5 | BQ356197 | BQ356197 | PM3-HT130 |
|   | 291 | 158.2 | 5.0 | 724  | 4 | BG716692 | BG716692 | 602678071 |
|   | 292 | 157   | 5.0 | 902  | 5 | BQ933408 | BQ933408 | AGENCOURT |
| c | 293 | 154.8 | 4.9 | 571  | 6 | CB438091 | CB438091 | 686532 MA |

|   |     |       |     |      |   |          |                    |
|---|-----|-------|-----|------|---|----------|--------------------|
|   | 294 | 154.6 | 4.9 | 473  | 4 | BI775884 | BI775884 468605 MA |
|   | 295 | 153.8 | 4.9 | 164  | 7 | D45630   | D45630 HUMGS02826  |
| c | 296 | 153.8 | 4.9 | 626  | 6 | CB431656 | CB431656 607652 MA |
| c | 297 | 153.6 | 4.9 | 582  | 6 | CB535123 | CB535123 768510 MA |
|   | 298 | 153.2 | 4.9 | 863  | 1 | AI323192 | AI323192 mp55g10.y |
|   | 299 | 152   | 4.8 | 745  | 5 | BM962964 | BM962964 UI-M-EQ0- |
| c | 300 | 151.6 | 4.8 | 172  | 2 | AW467911 | AW467911 he28c12.x |
|   | 301 | 150.2 | 4.8 | 780  | 7 | CN255480 | CN255480 170005312 |
|   | 302 | 149.8 | 4.8 | 615  | 1 | AL677440 | AL677440 AL677440  |
|   | 303 | 149   | 4.7 | 834  | 5 | BQ216757 | BQ216757 AGENCOURT |
|   | 304 | 146.4 | 4.7 | 977  | 5 | BX370082 | BX370082 BX370082  |
|   | 305 | 146   | 4.6 | 211  | 4 | BI345631 | BI345631 374509 MA |
|   | 306 | 146   | 4.6 | 886  | 5 | BQ943608 | BQ943608 AGENCOURT |
|   | 307 | 145.8 | 4.6 | 448  | 2 | BB847529 | BB847529 BB847529  |
|   | 308 | 145   | 4.6 | 416  | 2 | AW430454 | AW430454 70020 MAR |
|   | 309 | 143.8 | 4.6 | 615  | 6 | CB437039 | CB437039 684474 MA |
|   | 310 | 143.6 | 4.6 | 175  | 2 | AW313646 | AW313646 9051 MARC |
|   | 311 | 141.8 | 4.5 | 1068 | 4 | BM811543 | BM811543 AGENCOURT |
|   | 312 | 141.4 | 4.5 | 926  | 5 | BU909663 | BU909663 AGENCOURT |
|   | 313 | 141   | 4.5 | 706  | 7 | CN255488 | CN255488 170006001 |
|   | 314 | 141   | 4.5 | 728  | 7 | CN255483 | CN255483 170005322 |
|   | 315 | 141   | 4.5 | 864  | 4 | BI518922 | BI518922 603061844 |
|   | 316 | 140   | 4.5 | 270  | 2 | BB608272 | BB608272 BB608272  |
|   | 317 | 140   | 4.5 | 568  | 7 | CN255489 | CN255489 170005322 |
|   | 318 | 136.8 | 4.4 | 443  | 5 | BY167445 | BY167445 BY167445  |
|   | 319 | 136.4 | 4.3 | 580  | 2 | BE752387 | BE752387 204762 MA |
|   | 320 | 134   | 4.3 | 160  | 7 | CO261051 | CO261051 4133142 B |
|   | 321 | 134   | 4.3 | 948  | 5 | BQ685036 | BQ685036 AGENCOURT |
|   | 322 | 133   | 4.2 | 770  | 7 | CO248318 | CO248318 AGENCOURT |
| c | 323 | 132.2 | 4.2 | 573  | 2 | AW118237 | AW118237 xe12b08.x |
| c | 324 | 131.4 | 4.2 | 467  | 1 | AV617760 | AV617760 AV617760  |
|   | 325 | 131.4 | 4.2 | 615  | 5 | BM945001 | BM945001 UI-M-EH0p |
|   | 326 | 130.4 | 4.1 | 563  | 6 | CD216221 | CD216221 pgp2n.pk0 |
|   | 327 | 130.4 | 4.1 | 700  | 1 | AA763586 | AA763586 vp07g05.r |
| c | 328 | 130   | 4.1 | 561  | 4 | BM252112 | BM252112 BOTL01000 |
|   | 329 | 129.8 | 4.1 | 614  | 4 | BG712158 | BG712158 pg11n.pk0 |
|   | 330 | 129.6 | 4.1 | 418  | 2 | BE679181 | BE679181 dc60b02.y |
| c | 331 | 129.6 | 4.1 | 547  | 4 | BM220500 | BM220500 C0941F04- |
| c | 332 | 129.6 | 4.1 | 598  | 2 | BF714461 | BF714461 mab01a06. |
|   | 333 | 129.6 | 4.1 | 700  | 6 | BY763889 | BY763889 BY763889  |
| c | 334 | 129.6 | 4.1 | 711  | 5 | BP765487 | BP765487 BP765487  |
| c | 335 | 129.6 | 4.1 | 773  | 1 | AI132332 | AI132332 ue23g10.x |
| c | 336 | 129.6 | 4.1 | 780  | 7 | CO040927 | CO040927 UI-M-EV0- |
|   | 337 | 129.2 | 4.1 | 678  | 6 | CA041134 | CA041134 ssalshc50 |
|   | 338 | 129.2 | 4.1 | 3763 | 3 | AK088653 | AK088653 Mus muscu |
|   | 339 | 128.8 | 4.1 | 708  | 7 | CN789123 | CN789123 4123542 B |
|   | 340 | 128.2 | 4.1 | 372  | 6 | BY540732 | BY540732 BY540732  |
|   | 341 | 128   | 4.1 | 674  | 2 | BB045065 | BB045065 BB045065  |
|   | 342 | 127.2 | 4.0 | 290  | 2 | AW656129 | AW656129 108203 MA |
| c | 343 | 127   | 4.0 | 601  | 5 | BP768508 | BP768508 BP768508  |
|   | 344 | 126.8 | 4.0 | 625  | 2 | BE077531 | BE077531 RC1-BT060 |
|   | 345 | 126.6 | 4.0 | 342  | 1 | AA611491 | AA611491 vo89a05.r |
|   | 346 | 126.6 | 4.0 | 403  | 6 | BY540418 | BY540418 BY540418  |
|   | 347 | 126.2 | 4.0 | 426  | 2 | BB824296 | BB824296 BB824296  |
|   | 348 | 126.2 | 4.0 | 435  | 5 | BY517409 | BY517409 BY517409  |
|   | 349 | 125.8 | 4.0 | 593  | 6 | CD216085 | CD216085 pgp2n.pk0 |
|   | 350 | 125.6 | 4.0 | 387  | 5 | BY504344 | BY504344 BY504344  |

|   |     |       |     |     |   |          |          |           |
|---|-----|-------|-----|-----|---|----------|----------|-----------|
|   | 351 | 125.6 | 4.0 | 410 | 5 | BY510171 | BY510171 | BY510171  |
|   | 352 | 125.6 | 4.0 | 422 | 5 | BY494879 | BY494879 | BY494879  |
|   | 353 | 125.4 | 4.0 | 455 | 7 | CN223958 | CN223958 | WLA052D09 |
|   | 354 | 125.2 | 4.0 | 306 | 2 | AW436384 | AW436384 | 76556 MAR |
|   | 355 | 125.2 | 4.0 | 344 | 1 | AA611501 | AA611501 | vo89b04.r |
|   | 356 | 125.2 | 4.0 | 355 | 1 | AA823216 | AA823216 | vw42b01.r |
|   | 357 | 125.2 | 4.0 | 366 | 2 | BB792067 | BB792067 | BB792067  |
| c | 358 | 125.2 | 4.0 | 386 | 5 | BX639014 | BX639014 | BX639014  |
| c | 359 | 125.2 | 4.0 | 396 | 2 | BE851923 | BE851923 | uw18f07.x |
|   | 360 | 125.2 | 4.0 | 404 | 6 | BY575062 | BY575062 | BY575062  |
|   | 361 | 125.2 | 4.0 | 405 | 6 | BY625364 | BY625364 | BY625364  |
|   | 362 | 125.2 | 4.0 | 408 | 6 | BY547045 | BY547045 | BY547045  |
|   | 363 | 125.2 | 4.0 | 409 | 2 | BB743231 | BB743231 | BB743231  |
|   | 364 | 125.2 | 4.0 | 414 | 6 | BY538798 | BY538798 | BY538798  |
|   | 365 | 125.2 | 4.0 | 428 | 6 | BY579800 | BY579800 | BY579800  |
|   | 366 | 125.2 | 4.0 | 434 | 6 | BY551281 | BY551281 | BY551281  |
|   | 367 | 125.2 | 4.0 | 437 | 6 | BY523338 | BY523338 | BY523338  |
| c | 368 | 125.2 | 4.0 | 441 | 2 | AW061291 | AW061291 | UI-M-BH1- |
|   | 369 | 125.2 | 4.0 | 449 | 6 | BY546162 | BY546162 | BY546162  |
|   | 370 | 125.2 | 4.0 | 466 | 2 | BB731279 | BB731279 | BB731279  |
|   | 371 | 125.2 | 4.0 | 469 | 2 | BB824926 | BB824926 | BB824926  |
|   | 372 | 125.2 | 4.0 | 492 | 2 | AW493316 | AW493316 | UI-M-BH3- |
| c | 373 | 125.2 | 4.0 | 507 | 2 | AW060306 | AW060306 | UI-M-BH1- |
| c | 374 | 125.2 | 4.0 | 514 | 2 | BF020082 | BF020082 | ux14b02.x |
| c | 375 | 125.2 | 4.0 | 516 | 1 | AI098213 | AI098213 | ue27f05.x |
| c | 376 | 125.2 | 4.0 | 546 | 1 | AI323581 | AI323581 | mp55g10.x |
|   | 377 | 125.2 | 4.0 | 910 | 5 | BU552547 | BU552547 | AGENCOURT |
|   | 378 | 124.8 | 4.0 | 768 | 7 | CN255481 | CN255481 | 170005331 |
|   | 379 | 124.4 | 4.0 | 372 | 5 | BY236908 | BY236908 | BY236908  |
|   | 380 | 124.2 | 4.0 | 387 | 5 | BY511124 | BY511124 | BY511124  |
|   | 381 | 124.2 | 4.0 | 685 | 6 | CA371810 | CA371810 | 652409 NC |
|   | 382 | 124   | 3.9 | 396 | 6 | BY548006 | BY548006 | BY548006  |
| c | 383 | 124   | 3.9 | 446 | 1 | AI606228 | AI606228 | vn98f09.x |
|   | 384 | 123.8 | 3.9 | 314 | 2 | AW485003 | AW485003 | 63380 MAR |
|   | 385 | 123.8 | 3.9 | 862 | 5 | BQ224734 | BQ224734 | AGENCOURT |
|   | 386 | 123.6 | 3.9 | 399 | 6 | BY541776 | BY541776 | BY541776  |
|   | 387 | 123.6 | 3.9 | 410 | 5 | BY513291 | BY513291 | BY513291  |
|   | 388 | 123.6 | 3.9 | 433 | 5 | BY498637 | BY498637 | BY498637  |
|   | 389 | 123.6 | 3.9 | 660 | 2 | BB126942 | BB126942 | BB126942  |
|   | 390 | 123.6 | 3.9 | 853 | 7 | CR574223 | CR574223 | CR574223  |
|   | 391 | 123.4 | 3.9 | 319 | 2 | BB317324 | BB317324 | BB317324  |
|   | 392 | 123.2 | 3.9 | 406 | 5 | BY516094 | BY516094 | BY516094  |
| c | 393 | 123.2 | 3.9 | 446 | 5 | BP754487 | BP754487 | BP754487  |
|   | 394 | 123.2 | 3.9 | 655 | 4 | BJ618310 | BJ618310 | BJ618310  |
|   | 395 | 123   | 3.9 | 330 | 2 | BB164759 | BB164759 | BB164759  |
|   | 396 | 123   | 3.9 | 446 | 2 | BB820315 | BB820315 | BB820315  |
|   | 397 | 122.8 | 3.9 | 236 | 2 | BF776808 | BF776808 | 288536 MA |
|   | 398 | 122.8 | 3.9 | 851 | 7 | CF243117 | CF243117 | AGENCOURT |
|   | 399 | 122.8 | 3.9 | 880 | 5 | BU541109 | BU541109 | AGENCOURT |
|   | 400 | 122.6 | 3.9 | 399 | 6 | BY658194 | BY658194 | BY658194  |
|   | 401 | 122.6 | 3.9 | 405 | 2 | BB739127 | BB739127 | BB739127  |
|   | 402 | 122.6 | 3.9 | 414 | 2 | BE849780 | BE849780 | uw18f07.y |
|   | 403 | 122.6 | 3.9 | 417 | 5 | BY516312 | BY516312 | BY516312  |
|   | 404 | 122.6 | 3.9 | 432 | 6 | BY525070 | BY525070 | BY525070  |
|   | 405 | 122.6 | 3.9 | 445 | 2 | BB779387 | BB779387 | BB779387  |
|   | 406 | 122.4 | 3.9 | 399 | 5 | BY183603 | BY183603 | BY183603  |
|   | 407 | 122.4 | 3.9 | 401 | 5 | BY507720 | BY507720 | BY507720  |

|   |     |       |     |     |   |          |          |           |
|---|-----|-------|-----|-----|---|----------|----------|-----------|
|   | 408 | 122.2 | 3.9 | 343 | 2 | BB222788 | BB222788 | BB222788  |
|   | 409 | 122.2 | 3.9 | 415 | 6 | BY646549 | BY646549 | BY646549  |
|   | 410 | 122.2 | 3.9 | 420 | 6 | BY524914 | BY524914 | BY524914  |
| c | 411 | 122.2 | 3.9 | 515 | 4 | BM390926 | BM390926 | UI-R-CN1- |
|   | 412 | 122   | 3.9 | 347 | 2 | BB113642 | BB113642 | BB113642  |
|   | 413 | 122   | 3.9 | 402 | 5 | BY507653 | BY507653 | BY507653  |
|   | 414 | 121.8 | 3.9 | 314 | 1 | AV235779 | AV235779 | AV235779  |
|   | 415 | 121.8 | 3.9 | 548 | 2 | BF039888 | BF039888 | BP250025A |
|   | 416 | 121.8 | 3.9 | 932 | 5 | BX369159 | BX369159 | BX369159  |
|   | 417 | 121.6 | 3.9 | 623 | 4 | BJ095128 | BJ095128 | BJ095128  |
|   | 418 | 121.6 | 3.9 | 881 | 4 | BG824522 | BG824522 | 602727494 |
| c | 419 | 121.4 | 3.9 | 651 | 4 | BM385797 | BM385797 | UI-R-CN1- |
|   | 420 | 121.2 | 3.9 | 358 | 5 | BY205630 | BY205630 | BY205630  |
|   | 421 | 121.2 | 3.9 | 872 | 4 | BG831590 | BG831590 | 602765850 |
| c | 422 | 121   | 3.8 | 293 | 7 | CO988317 | CO988317 | UMC-pd3en |
| c | 423 | 121   | 3.8 | 387 | 2 | BE690913 | BE690913 | uw60d09.x |
|   | 424 | 120.8 | 3.8 | 336 | 2 | BB219364 | BB219364 | BB219364  |
|   | 425 | 120.8 | 3.8 | 589 | 4 | BI391274 | BI391274 | pgpln.pk0 |
|   | 426 | 120.6 | 3.8 | 351 | 2 | BE668250 | BE668250 | 156853 MA |
| c | 427 | 120.6 | 3.8 | 431 | 6 | CA945768 | CA945768 | UI-R-FS1- |
| c | 428 | 120.6 | 3.8 | 435 | 1 | AI454122 | AI454122 | UI-R-BT0- |
| c | 429 | 120.6 | 3.8 | 473 | 2 | AW523699 | AW523699 | UI-R-BO0- |
| c | 430 | 120.6 | 3.8 | 552 | 2 | BE110750 | BE110750 | UI-R-BJ1- |
| c | 431 | 120.6 | 3.8 | 555 | 5 | BQ190381 | BQ190381 | UI-R-DN1- |
| c | 432 | 120.6 | 3.8 | 649 | 6 | CB322846 | CB322846 | UI-R-DY0- |
|   | 433 | 120.4 | 3.8 | 328 | 2 | BB223967 | BB223967 | BB223967  |
|   | 434 | 120.4 | 3.8 | 377 | 6 | BY630131 | BY630131 | BY630131  |
|   | 435 | 120.4 | 3.8 | 424 | 5 | BY378169 | BY378169 | BY378169  |
| c | 436 | 120.4 | 3.8 | 528 | 5 | BQ031863 | BQ031863 | UI-1-CF0- |
| c | 437 | 120.2 | 3.8 | 381 | 7 | CR468045 | CR468045 | CR468045  |
|   | 438 | 120.2 | 3.8 | 446 | 1 | AA254731 | AA254731 | mz80h03.r |
|   | 439 | 120.2 | 3.8 | 486 | 6 | BY591764 | BY591764 | BY591764  |
| c | 440 | 120.2 | 3.8 | 656 | 4 | BM251667 | BM251667 | BOTL01000 |
|   | 441 | 120   | 3.8 | 324 | 2 | BB503600 | BB503600 | BB503600  |
|   | 442 | 120   | 3.8 | 904 | 5 | BU543096 | BU543096 | AGENCOURT |
|   | 443 | 119.8 | 3.8 | 317 | 2 | BB828413 | BB828413 | BB828413  |
|   | 444 | 119.8 | 3.8 | 414 | 5 | BY498892 | BY498892 | BY498892  |
|   | 445 | 119.4 | 3.8 | 325 | 2 | BB392255 | BB392255 | BB392255  |
|   | 446 | 119.4 | 3.8 | 333 | 1 | AA755192 | AA755192 | vq62b08.r |
|   | 447 | 119.4 | 3.8 | 447 | 6 | BY539681 | BY539681 | BY539681  |
|   | 448 | 119.2 | 3.8 | 329 | 2 | BB321099 | BB321099 | BB321099  |
|   | 449 | 119.2 | 3.8 | 961 | 5 | BU542955 | BU542955 | AGENCOURT |
|   | 450 | 119   | 3.8 | 262 | 2 | AW313948 | AW313948 | 9649 MARC |
|   | 451 | 119   | 3.8 | 262 | 2 | AW477528 | AW477528 | 13351 MAR |
|   | 452 | 118.6 | 3.8 | 316 | 2 | BB210291 | BB210291 | BB210291  |
|   | 453 | 118.4 | 3.8 | 422 | 5 | BY509778 | BY509778 | BY509778  |
|   | 454 | 118.4 | 3.8 | 808 | 5 | BU187281 | BU187281 | AGENCOURT |
| c | 455 | 118.2 | 3.8 | 392 | 4 | BI290997 | BI290997 | UI-R-DK0- |
|   | 456 | 118.2 | 3.8 | 670 | 7 | CK834036 | CK834036 | 4058164 B |
|   | 457 | 118.2 | 3.8 | 779 | 7 | CF288502 | CF288502 | AGENCOURT |
|   | 458 | 118   | 3.8 | 373 | 5 | BY017370 | BY017370 | BY017370  |
| c | 459 | 118   | 3.8 | 428 | 6 | CB059945 | CB059945 | 4010160 B |
|   | 460 | 118   | 3.8 | 763 | 5 | BU612234 | BU612234 | UI-M-EW0- |
|   | 461 | 117.8 | 3.7 | 409 | 5 | BY506868 | BY506868 | BY506868  |
|   | 462 | 117.6 | 3.7 | 325 | 2 | BB138812 | BB138812 | BB138812  |
|   | 463 | 117.6 | 3.7 | 329 | 2 | BB560121 | BB560121 | BB560121  |
|   | 464 | 117.6 | 3.7 | 453 | 6 | CB060019 | CB060019 | 4010021 B |

|   |     |       |     |      |   |          |          |           |
|---|-----|-------|-----|------|---|----------|----------|-----------|
|   | 465 | 117.6 | 3.7 | 654  | 5 | BP754486 | BP754486 | BP754486  |
|   | 466 | 117.4 | 3.7 | 504  | 1 | AA110742 | AA110742 | mp55g10.r |
|   | 467 | 117.4 | 3.7 | 726  | 7 | CK980025 | CK980025 | 4111598 B |
|   | 468 | 117.2 | 3.7 | 336  | 2 | BB165167 | BB165167 | BB165167  |
|   | 469 | 117.2 | 3.7 | 407  | 5 | BY516195 | BY516195 | BY516195  |
|   | 470 | 117   | 3.7 | 149  | 6 | CB062937 | CB062937 | 4013191 B |
|   | 471 | 117   | 3.7 | 315  | 2 | BB269712 | BB269712 | BB269712  |
|   | 472 | 117   | 3.7 | 738  | 1 | AL702888 | AL702888 | DKFZp686D |
|   | 473 | 117   | 3.7 | 917  | 5 | BU916713 | BU916713 | AGENCOURT |
|   | 474 | 116.8 | 3.7 | 322  | 2 | BB220489 | BB220489 | BB220489  |
|   | 475 | 116.6 | 3.7 | 412  | 6 | CB802007 | CB802007 | AMGNNUC:N |
|   | 476 | 116.6 | 3.7 | 426  | 2 | AW767390 | AW767390 | da68e03.y |
|   | 477 | 116.6 | 3.7 | 711  | 7 | CN401142 | CN401142 | 170005328 |
|   | 478 | 116.6 | 3.7 | 933  | 4 | BG424061 | BG424061 | 602448130 |
| c | 479 | 116.2 | 3.7 | 689  | 5 | BX885697 | BX885697 | BX885697  |
|   | 480 | 116   | 3.7 | 413  | 5 | BY516984 | BY516984 | BY516984  |
|   | 481 | 115.8 | 3.7 | 315  | 2 | BB217943 | BB217943 | BB217943  |
|   | 482 | 115.6 | 3.7 | 308  | 2 | BB226784 | BB226784 | BB226784  |
|   | 483 | 115.6 | 3.7 | 459  | 6 | BY596859 | BY596859 | BY596859  |
|   | 484 | 115.4 | 3.7 | 328  | 2 | BB203677 | BB203677 | BB203677  |
|   | 485 | 115   | 3.7 | 653  | 4 | BG423200 | BG423200 | 602450518 |
|   | 486 | 115   | 3.7 | 1045 | 5 | BX458922 | BX458922 | BX458922  |
|   | 487 | 114.8 | 3.7 | 865  | 5 | BQ962412 | BQ962412 | AGENCOURT |
|   | 488 | 114.6 | 3.6 | 413  | 6 | BY577648 | BY577648 | BY577648  |
|   | 489 | 114.4 | 3.6 | 318  | 2 | BB221006 | BB221006 | BB221006  |
|   | 490 | 114.4 | 3.6 | 3226 | 3 | AK042751 | AK042751 | Mus muscu |
|   | 491 | 114.4 | 3.6 | 3329 | 3 | AK082711 | AK082711 | Mus muscu |
|   | 492 | 114   | 3.6 | 268  | 2 | BB594900 | BB594900 | BB594900  |
|   | 493 | 113.8 | 3.6 | 552  | 7 | CN664343 | CN664343 | A0811H09- |
|   | 494 | 113.4 | 3.6 | 408  | 5 | BY159825 | BY159825 | BY159825  |
|   | 495 | 113.4 | 3.6 | 1035 | 5 | BQ944697 | BQ944697 | AGENCOURT |
|   | 496 | 113.2 | 3.6 | 262  | 2 | BB733435 | BB733435 | BB733435  |
|   | 497 | 113.2 | 3.6 | 297  | 2 | BB082267 | BB082267 | BB082267  |
|   | 498 | 113   | 3.6 | 294  | 2 | BB369725 | BB369725 | BB369725  |
|   | 499 | 113   | 3.6 | 311  | 2 | BB319473 | BB319473 | BB319473  |
|   | 500 | 113   | 3.6 | 647  | 4 | BI159977 | BI159977 | 602863854 |
|   | 501 | 112.8 | 3.6 | 286  | 2 | BB180038 | BB180038 | BB180038  |
|   | 502 | 112.8 | 3.6 | 339  | 2 | BB137126 | BB137126 | BB137126  |
|   | 503 | 112.2 | 3.6 | 339  | 2 | BB224502 | BB224502 | BB224502  |
|   | 504 | 112.2 | 3.6 | 341  | 2 | BB224286 | BB224286 | BB224286  |
|   | 505 | 112.2 | 3.6 | 470  | 2 | BB822561 | BB822561 | BB822561  |
|   | 506 | 112   | 3.6 | 298  | 2 | BB360425 | BB360425 | BB360425  |
|   | 507 | 112   | 3.6 | 316  | 2 | BB218778 | BB218778 | BB218778  |
|   | 508 | 112   | 3.6 | 940  | 4 | BG386070 | BG386070 | 602455244 |
|   | 509 | 111.8 | 3.6 | 287  | 2 | BB179402 | BB179402 | BB179402  |
|   | 510 | 111.8 | 3.6 | 395  | 5 | BY019515 | BY019515 | BY019515  |
|   | 511 | 111.8 | 3.6 | 691  | 4 | BG422155 | BG422155 | 602448882 |
|   | 512 | 111.6 | 3.6 | 300  | 2 | BB522135 | BB522135 | BB522135  |
|   | 513 | 111.6 | 3.6 | 307  | 2 | BB116702 | BB116702 | BB116702  |
|   | 514 | 111.4 | 3.5 | 321  | 2 | BB236584 | BB236584 | BB236584  |
|   | 515 | 111.4 | 3.5 | 338  | 2 | BB120467 | BB120467 | BB120467  |
|   | 516 | 111.2 | 3.5 | 286  | 2 | BB222636 | BB222636 | BB222636  |
|   | 517 | 111.2 | 3.5 | 304  | 2 | BB219012 | BB219012 | BB219012  |
|   | 518 | 111.2 | 3.5 | 306  | 1 | AV239830 | AV239830 | AV239830  |
|   | 519 | 111.2 | 3.5 | 678  | 4 | BM495316 | BM495316 | IpCGBr2_2 |
| c | 520 | 111.2 | 3.5 | 738  | 4 | BM414643 | BM414643 | ECC00109  |
|   | 521 | 111   | 3.5 | 277  | 2 | BB324525 | BB324525 | BB324525  |



|   |     |       |     |      |   |          |          |           |
|---|-----|-------|-----|------|---|----------|----------|-----------|
|   | 522 | 110.8 | 3.5 | 295  | 2 | BB511397 | BB511397 | BB511397  |
|   | 523 | 110.6 | 3.5 | 1606 | 2 | BF581604 | BF581604 | 602099944 |
|   | 524 | 110.4 | 3.5 | 788  | 4 | BI161171 | BI161171 | 602865624 |
|   | 525 | 110.2 | 3.5 | 334  | 2 | BB224542 | BB224542 | BB224542  |
|   | 526 | 110   | 3.5 | 288  | 2 | BB346214 | BB346214 | BB346214  |
|   | 527 | 110   | 3.5 | 310  | 2 | BB265127 | BB265127 | BB265127  |
| c | 528 | 110   | 3.5 | 344  | 1 | AI070233 | AI070233 | UI-R-Y0-1 |
|   | 529 | 109.8 | 3.5 | 306  | 2 | BB530000 | BB530000 | BB530000  |
|   | 530 | 109.8 | 3.5 | 487  | 7 | CN367763 | CN367763 | 170005322 |
|   | 531 | 109.6 | 3.5 | 284  | 2 | BB733429 | BB733429 | BB733429  |
|   | 532 | 109.6 | 3.5 | 293  | 2 | BB334189 | BB334189 | BB334189  |
|   | 533 | 109.6 | 3.5 | 452  | 6 | BY588670 | BY588670 | BY588670  |
|   | 534 | 109.4 | 3.5 | 317  | 1 | AV102365 | AV102365 | AV102365  |
|   | 535 | 109.4 | 3.5 | 826  | 5 | BU175920 | BU175920 | AGENCOURT |
|   | 536 | 109.4 | 3.5 | 1132 | 6 | CD504092 | CD504092 | CDA66-A08 |
|   | 537 | 109.2 | 3.5 | 357  | 5 | BY193799 | BY193799 | BY193799  |
|   | 538 | 109   | 3.5 | 110  | 6 | CD631366 | CD631366 | 56027747J |
|   | 539 | 109   | 3.5 | 292  | 2 | BB440274 | BB440274 | BB440274  |
|   | 540 | 109   | 3.5 | 295  | 2 | BB179256 | BB179256 | BB179256  |
|   | 541 | 109   | 3.5 | 298  | 2 | BB257753 | BB257753 | BB257753  |
|   | 542 | 108.8 | 3.5 | 309  | 2 | BB124269 | BB124269 | BB124269  |
|   | 543 | 108.8 | 3.5 | 310  | 2 | BB335680 | BB335680 | BB335680  |
| c | 544 | 108.6 | 3.5 | 457  | 2 | BE686664 | BE686664 | uw03e06.x |
|   | 545 | 108.4 | 3.4 | 292  | 2 | BB173217 | BB173217 | BB173217  |
|   | 546 | 108.4 | 3.4 | 299  | 2 | BB276146 | BB276146 | BB276146  |
|   | 547 | 108.2 | 3.4 | 168  | 2 | AW345212 | AW345212 | 25329 MAR |
|   | 548 | 108.2 | 3.4 | 311  | 2 | BB143870 | BB143870 | BB143870  |
|   | 549 | 108.2 | 3.4 | 910  | 4 | BI161349 | BI161349 | 602865754 |
|   | 550 | 108   | 3.4 | 290  | 2 | BB278479 | BB278479 | BB278479  |
|   | 551 | 108   | 3.4 | 303  | 2 | BB217218 | BB217218 | BB217218  |
|   | 552 | 108   | 3.4 | 949  | 5 | BU541977 | BU541977 | AGENCOURT |
|   | 553 | 108   | 3.4 | 3137 | 3 | BC051979 | BC051979 | Mus muscu |
|   | 554 | 108   | 3.4 | 3907 | 3 | AK031131 | AK031131 | Mus muscu |
| c | 555 | 107.8 | 3.4 | 557  | 1 | AU147993 | AU147993 | AU147993  |
|   | 556 | 107.6 | 3.4 | 689  | 7 | CO434547 | CO434547 | UI-M-HX0- |
|   | 557 | 107.6 | 3.4 | 1141 | 6 | CA975355 | CA975355 | AGENCOURT |
|   | 558 | 107.4 | 3.4 | 289  | 2 | BB007231 | BB007231 | BB007231  |
|   | 559 | 107.4 | 3.4 | 305  | 2 | BB500334 | BB500334 | BB500334  |
| c | 560 | 107.4 | 3.4 | 436  | 1 | AA913136 | AA913136 | oi17h07.s |
|   | 561 | 107.4 | 3.4 | 569  | 7 | CO258909 | CO258909 | 4130136 B |
| c | 562 | 107.4 | 3.4 | 734  | 5 | BX674351 | BX674351 | BX674351  |
|   | 563 | 107.2 | 3.4 | 312  | 2 | BB445664 | BB445664 | BB445664  |
|   | 564 | 107   | 3.4 | 284  | 2 | BB507939 | BB507939 | BB507939  |
|   | 565 | 106.8 | 3.4 | 289  | 2 | BB496529 | BB496529 | BB496529  |
|   | 566 | 106.8 | 3.4 | 290  | 2 | BB368263 | BB368263 | BB368263  |
|   | 567 | 106.8 | 3.4 | 292  | 2 | BB354765 | BB354765 | BB354765  |
|   | 568 | 106.8 | 3.4 | 304  | 2 | BB336700 | BB336700 | BB336700  |
|   | 569 | 106.8 | 3.4 | 328  | 2 | BB220954 | BB220954 | BB220954  |
|   | 570 | 106.6 | 3.4 | 686  | 4 | BG469296 | BG469296 | 602533135 |
|   | 571 | 106.4 | 3.4 | 279  | 2 | BB371226 | BB371226 | BB371226  |
|   | 572 | 106.4 | 3.4 | 286  | 2 | BB555504 | BB555504 | BB555504  |
|   | 573 | 106.4 | 3.4 | 294  | 1 | AV051876 | AV051876 | AV051876  |
|   | 574 | 106.4 | 3.4 | 336  | 2 | AW226731 | AW226731 | um60b09.y |
| c | 575 | 106.4 | 3.4 | 488  | 4 | BM151697 | BM151697 | TCBAP1E10 |
|   | 576 | 106.2 | 3.4 | 281  | 2 | BB346087 | BB346087 | BB346087  |
|   | 577 | 106.2 | 3.4 | 725  | 7 | CN429157 | CN429157 | 170004252 |
|   | 578 | 106   | 3.4 | 306  | 2 | BB262651 | BB262651 | BB262651  |

|       |       |     |      |   |          |          |           |
|-------|-------|-----|------|---|----------|----------|-----------|
| 579   | 106   | 3.4 | 318  | 2 | BB243620 | BB243620 | BB243620  |
| 580   | 105.8 | 3.4 | 272  | 2 | BB552255 | BB552255 | BB552255  |
| 581   | 105.8 | 3.4 | 283  | 2 | BB128450 | BB128450 | BB128450  |
| 582   | 105.8 | 3.4 | 292  | 2 | BB500569 | BB500569 | BB500569  |
| 583   | 105.8 | 3.4 | 976  | 5 | BQ944147 | BQ944147 | AGENCOURT |
| 584   | 105.6 | 3.4 | 281  | 2 | BB348185 | BB348185 | BB348185  |
| 585   | 105.6 | 3.4 | 811  | 6 | CD653578 | CD653578 | AGENCOURT |
| 586   | 105.6 | 3.4 | 824  | 4 | BM047429 | BM047429 | 603628715 |
| 587   | 105.6 | 3.4 | 900  | 4 | BG326356 | BG326356 | 602425281 |
| 588   | 105.4 | 3.4 | 363  | 6 | CD631362 | CD631362 | 56027755J |
| c 589 | 105.4 | 3.4 | 603  | 7 | CK849657 | CK849657 | 972704 BA |
| c 590 | 105.4 | 3.4 | 742  | 5 | BX910552 | BX910552 | BX910552  |
| 591   | 105.2 | 3.3 | 287  | 2 | BB325091 | BB325091 | BB325091  |
| 592   | 105   | 3.3 | 394  | 6 | CB776364 | CB776364 | AMGNNUC:N |
| 593   | 105   | 3.3 | 860  | 5 | BQ230111 | BQ230111 | AGENCOURT |
| 594   | 105   | 3.3 | 924  | 4 | BG326746 | BG326746 | 602425623 |
| 595   | 105   | 3.3 | 963  | 5 | BU552403 | BU552403 | AGENCOURT |
| 596   | 105   | 3.3 | 1024 | 2 | BE910319 | BE910319 | 601503675 |
| 597   | 104.8 | 3.3 | 262  | 1 | AV241169 | AV241169 | AV241169  |
| 598   | 104.8 | 3.3 | 306  | 2 | BB500200 | BB500200 | BB500200  |
| 599   | 104.8 | 3.3 | 414  | 2 | BB826095 | BB826095 | BB826095  |
| 600   | 104.8 | 3.3 | 795  | 6 | CB245479 | CB245479 | UI-M-FY0- |
| 601   | 104.8 | 3.3 | 911  | 5 | BU501900 | BU501900 | AGENCOURT |
| 602   | 104.8 | 3.3 | 919  | 5 | BU173969 | BU173969 | AGENCOURT |
| 603   | 104.6 | 3.3 | 282  | 2 | BB532703 | BB532703 | BB532703  |
| 604   | 104.6 | 3.3 | 309  | 2 | BB499049 | BB499049 | BB499049  |
| 605   | 104.2 | 3.3 | 310  | 2 | BB236046 | BB236046 | BB236046  |
| 606   | 104.2 | 3.3 | 328  | 2 | BB114323 | BB114323 | BB114323  |
| 607   | 104.2 | 3.3 | 414  | 6 | BY578439 | BY578439 | BY578439  |
| 608   | 104.2 | 3.3 | 897  | 5 | BQ219988 | BQ219988 | AGENCOURT |
| 609   | 104.2 | 3.3 | 927  | 4 | BG831583 | BG831583 | 602765840 |
| 610   | 104   | 3.3 | 266  | 2 | BB716868 | BB716868 | BB716868  |
| 611   | 104   | 3.3 | 283  | 2 | BB528644 | BB528644 | BB528644  |
| 612   | 104   | 3.3 | 288  | 2 | BB342818 | BB342818 | BB342818  |
| 613   | 104   | 3.3 | 2855 | 3 | AK047067 | AK047067 | Mus muscu |
| 614   | 103.8 | 3.3 | 298  | 2 | BB283107 | BB283107 | BB283107  |
| 615   | 103.8 | 3.3 | 879  | 4 | BG831929 | BG831929 | 602765589 |
| 616   | 103.6 | 3.3 | 297  | 2 | BB217129 | BB217129 | BB217129  |
| 617   | 103.6 | 3.3 | 307  | 2 | BB500311 | BB500311 | BB500311  |
| 618   | 103.6 | 3.3 | 311  | 2 | BB533042 | BB533042 | BB533042  |
| 619   | 103.6 | 3.3 | 315  | 2 | BB122455 | BB122455 | BB122455  |
| 620   | 103.6 | 3.3 | 464  | 2 | BB796655 | BB796655 | BB796655  |
| 621   | 103.4 | 3.3 | 314  | 2 | BB239048 | BB239048 | BB239048  |
| 622   | 103.2 | 3.3 | 233  | 2 | BB510804 | BB510804 | BB510804  |
| 623   | 103.2 | 3.3 | 286  | 2 | BB178968 | BB178968 | BB178968  |
| 624   | 103.2 | 3.3 | 467  | 6 | BY556536 | BY556536 | BY556536  |
| 625   | 103.2 | 3.3 | 583  | 4 | BM488072 | BM488072 | pgm2n.pk0 |
| 626   | 103.2 | 3.3 | 868  | 1 | AU140366 | AU140366 | AU140366  |
| 627   | 103   | 3.3 | 282  | 2 | BB310767 | BB310767 | BB310767  |
| 628   | 103   | 3.3 | 619  | 1 | AL118624 | AL118624 | DKFZp761F |
| 629   | 102.8 | 3.3 | 269  | 2 | BB313946 | BB313946 | BB313946  |
| 630   | 102.6 | 3.3 | 271  | 2 | BB216188 | BB216188 | BB216188  |
| 631   | 102.6 | 3.3 | 579  | 5 | BP375801 | BP375801 | BP375801  |
| 632   | 102.6 | 3.3 | 869  | 5 | BM947242 | BM947242 | UI-M-EH0p |
| 633   | 102.6 | 3.3 | 977  | 5 | BU520216 | BU520216 | AGENCOURT |
| 634   | 102.4 | 3.3 | 281  | 2 | BB129002 | BB129002 | BB129002  |
| 635   | 102.2 | 3.3 | 268  | 2 | BB216101 | BB216101 | BB216101  |

|   |     |       |     |      |   |          |          |           |
|---|-----|-------|-----|------|---|----------|----------|-----------|
|   | 636 | 102.2 | 3.3 | 271  | 2 | BB555572 | BB555572 | BB555572  |
|   | 637 | 102.2 | 3.3 | 285  | 2 | BB324617 | BB324617 | BB324617  |
|   | 638 | 102.2 | 3.3 | 342  | 2 | BB223376 | BB223376 | BB223376  |
|   | 639 | 102.2 | 3.3 | 644  | 1 | AL803713 | AL803713 | AL803713  |
|   | 640 | 102.2 | 3.3 | 659  | 7 | CN695559 | CN695559 | E0366G09- |
| c | 641 | 102   | 3.2 | 331  | 1 | AI228417 | AI228417 | EST225112 |
|   | 642 | 102   | 3.2 | 426  | 5 | BY376368 | BY376368 | BY376368  |
| c | 643 | 102   | 3.2 | 654  | 6 | CB420254 | CB420254 | 593189 MA |
|   | 644 | 102   | 3.2 | 6875 | 3 | BC032619 | BC032619 | Homo sapi |
|   | 645 | 101.8 | 3.2 | 222  | 2 | BB150791 | BB150791 | BB150791  |
| c | 646 | 101.8 | 3.2 | 353  | 8 | BZ845553 | BZ845553 | CH240_213 |
| c | 647 | 101.8 | 3.2 | 538  | 8 | AQ434948 | AQ434948 | HS_5126_B |
|   | 648 | 101.8 | 3.2 | 779  | 5 | BX396978 | BX396978 | BX396978  |
|   | 649 | 101.8 | 3.2 | 1002 | 5 | BQ068313 | BQ068313 | AGENCOURT |
|   | 650 | 101.6 | 3.2 | 315  | 2 | BB116770 | BB116770 | BB116770  |
| c | 651 | 101.6 | 3.2 | 537  | 2 | BE349814 | BE349814 | hq43e01.x |
|   | 652 | 101.2 | 3.2 | 317  | 2 | BB213717 | BB213717 | BB213717  |
|   | 653 | 101   | 3.2 | 254  | 2 | BB172165 | BB172165 | BB172165  |
|   | 654 | 101   | 3.2 | 2719 | 3 | AK035993 | AK035993 | Mus muscu |
|   | 655 | 100.8 | 3.2 | 400  | 6 | BY555199 | BY555199 | BY555199  |
| c | 656 | 100.8 | 3.2 | 492  | 1 | AA023538 | AA023538 | mh75d07.r |
|   | 657 | 100.8 | 3.2 | 622  | 6 | CD349441 | CD349441 | UI-M-FY0- |
|   | 658 | 100.6 | 3.2 | 505  | 4 | BI898654 | BI898654 | 479668 MA |
|   | 659 | 100.6 | 3.2 | 651  | 4 | BM491746 | BM491746 | pgp2n.pk0 |
|   | 660 | 100.4 | 3.2 | 285  | 2 | BB177820 | BB177820 | BB177820  |
|   | 661 | 100.2 | 3.2 | 699  | 4 | BG830948 | BG830948 | 602766844 |
|   | 662 | 100.2 | 3.2 | 861  | 7 | CO735048 | CO735048 | SlLE04c10 |
|   | 663 | 100   | 3.2 | 224  | 2 | BB499666 | BB499666 | BB499666  |
|   | 664 | 100   | 3.2 | 286  | 2 | BB110106 | BB110106 | BB110106  |
|   | 665 | 100   | 3.2 | 316  | 2 | BB145363 | BB145363 | BB145363  |
| c | 666 | 100   | 3.2 | 582  | 2 | BF400607 | BF400607 | UI-R-CA0- |
|   | 667 | 100   | 3.2 | 786  | 7 | CK365293 | CK365293 | AGENCOURT |
|   | 668 | 99.8  | 3.2 | 313  | 2 | BB218103 | BB218103 | BB218103  |
|   | 669 | 99.8  | 3.2 | 594  | 7 | CN528682 | CN528682 | UI-M-HQ0- |
|   | 670 | 99.8  | 3.2 | 910  | 4 | BG470201 | BG470201 | 602533710 |
|   | 671 | 99.8  | 3.2 | 3921 | 3 | AK084922 | AK084922 | Mus muscu |
|   | 672 | 99.8  | 3.2 | 4374 | 3 | AK031307 | AK031307 | Mus muscu |
| c | 673 | 99.6  | 3.2 | 278  | 6 | CD631370 | CD631370 | 56027863J |
| c | 674 | 99.6  | 3.2 | 703  | 1 | AU170734 | AU170734 | AU170734  |
|   | 675 | 99.6  | 3.2 | 844  | 7 | CO735027 | CO735027 | SlLE04c10 |
|   | 676 | 99.6  | 3.2 | 880  | 5 | BU186709 | BU186709 | AGENCOURT |
|   | 677 | 99.4  | 3.2 | 286  | 2 | BB333313 | BB333313 | BB333313  |
|   | 678 | 99.4  | 3.2 | 772  | 4 | BG829652 | BG829652 | 602764012 |
|   | 679 | 99.2  | 3.2 | 275  | 2 | BB227524 | BB227524 | BB227524  |
|   | 680 | 99.2  | 3.2 | 326  | 2 | BB559836 | BB559836 | BB559836  |
|   | 681 | 99    | 3.1 | 239  | 1 | AV229642 | AV229642 | AV229642  |
|   | 682 | 99    | 3.1 | 264  | 1 | AV238667 | AV238667 | AV238667  |
|   | 683 | 99    | 3.1 | 316  | 2 | BB532106 | BB532106 | BB532106  |
| c | 684 | 99    | 3.1 | 319  | 4 | BG377549 | BG377549 | UI-R-CU0- |
|   | 685 | 98.6  | 3.1 | 121  | 1 | AI264258 | AI264258 | qk20b04.x |
|   | 686 | 98.6  | 3.1 | 278  | 2 | BB176510 | BB176510 | BB176510  |
|   | 687 | 98.6  | 3.1 | 317  | 1 | AL655823 | AL655823 | AL655823  |
|   | 688 | 98.4  | 3.1 | 100  | 4 | BI002468 | BI002468 | MR3-HN015 |
|   | 689 | 98.4  | 3.1 | 228  | 2 | BB150964 | BB150964 | BB150964  |
|   | 690 | 98.4  | 3.1 | 288  | 2 | BB455324 | BB455324 | BB455324  |
|   | 691 | 98.4  | 3.1 | 320  | 2 | BB242404 | BB242404 | BB242404  |
|   | 692 | 98.2  | 3.1 | 278  | 1 | AV313234 | AV313234 | AV313234  |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 693   | 98.2 | 3.1 | 308  | 2 | BB263999 | BB263999 | BB263999  |
| 694   | 98.2 | 3.1 | 668  | 6 | BY746861 | BY746861 | BY746861  |
| 695   | 98.2 | 3.1 | 4476 | 3 | AK052232 | AK052232 | Mus muscu |
| 696   | 98   | 3.1 | 235  | 2 | BB716819 | BB716819 | BB716819  |
| 697   | 98   | 3.1 | 280  | 2 | BB535881 | BB535881 | BB535881  |
| 698   | 97.6 | 3.1 | 203  | 4 | BM105287 | BM105287 | 508710 MA |
| 699   | 97.6 | 3.1 | 369  | 5 | BY020398 | BY020398 | BY020398  |
| 700   | 97.4 | 3.1 | 705  | 2 | BE294211 | BE294211 | 601172744 |
| 701   | 97.2 | 3.1 | 256  | 2 | BB425457 | BB425457 | BB425457  |
| 702   | 97.2 | 3.1 | 281  | 1 | AV235738 | AV235738 | AV235738  |
| 703   | 97.2 | 3.1 | 640  | 7 | CN460578 | CN460578 | UI-M-HB0- |
| 704   | 97.2 | 3.1 | 704  | 6 | BY741417 | BY741417 | BY741417  |
| 705   | 96.8 | 3.1 | 223  | 1 | AV229388 | AV229388 | AV229388  |
| 706   | 96.8 | 3.1 | 225  | 2 | BB323996 | BB323996 | BB323996  |
| 707   | 96.8 | 3.1 | 236  | 2 | BB019685 | BB019685 | BB019685  |
| 708   | 96.8 | 3.1 | 242  | 2 | BB554948 | BB554948 | BB554948  |
| 709   | 96.8 | 3.1 | 273  | 2 | BB010623 | BB010623 | BB010623  |
| 710   | 96.8 | 3.1 | 286  | 2 | BB309932 | BB309932 | BB309932  |
| 711   | 96.8 | 3.1 | 496  | 7 | CK390327 | CK390327 | K0817F12- |
| 712   | 96.8 | 3.1 | 815  | 4 | BG386811 | BG386811 | 602455071 |
| 713   | 96.8 | 3.1 | 986  | 4 | BG746534 | BG746534 | 602703833 |
| 714   | 96.8 | 3.1 | 1394 | 5 | BM926974 | BM926974 | AGENCOURT |
| 715   | 96.6 | 3.1 | 234  | 2 | BB357534 | BB357534 | BB357534  |
| 716   | 96.6 | 3.1 | 340  | 5 | BY353322 | BY353322 | BY353322  |
| 717   | 96.6 | 3.1 | 342  | 2 | BB241607 | BB241607 | BB241607  |
| 718   | 96.6 | 3.1 | 352  | 5 | BY177856 | BY177856 | BY177856  |
| 719   | 96.6 | 3.1 | 396  | 5 | BY201883 | BY201883 | BY201883  |
| 720   | 96.6 | 3.1 | 795  | 7 | CO571948 | CO571948 | AGENCOURT |
| 721   | 96.4 | 3.1 | 721  | 6 | CA324424 | CA324424 | UI-M-FY0- |
| 722   | 96.4 | 3.1 | 779  | 6 | CA316005 | CA316005 | UI-M-FW0- |
| c 723 | 96.2 | 3.1 | 297  | 1 | AI112352 | AI112352 | UI-R-Y0-m |
| c 724 | 96.2 | 3.1 | 297  | 1 | AI576402 | AI576402 | UI-R-Y0-v |
| 725   | 96.2 | 3.1 | 333  | 1 | AV006222 | AV006222 | AV006222  |
| 726   | 96   | 3.1 | 400  | 5 | BY158515 | BY158515 | BY158515  |
| 727   | 96   | 3.1 | 917  | 4 | BG324311 | BG324311 | 602423309 |
| 728   | 95.8 | 3.0 | 586  | 2 | BF041445 | BF041445 | BP250015B |
| 729   | 95.8 | 3.0 | 673  | 5 | BM951984 | BM951984 | UI-M-EH0- |
| c 730 | 95.8 | 3.0 | 710  | 7 | CK979615 | CK979615 | 4111214 B |
| 731   | 95.4 | 3.0 | 178  | 2 | BF774071 | BF774071 | 283623 MA |
| 732   | 95.4 | 3.0 | 178  | 2 | BF774072 | BF774072 | 283624 MA |
| 733   | 95.4 | 3.0 | 222  | 2 | BB052672 | BB052672 | BB052672  |
| 734   | 95.4 | 3.0 | 238  | 2 | BB034746 | BB034746 | BB034746  |
| 735   | 95.4 | 3.0 | 261  | 2 | BB594935 | BB594935 | BB594935  |
| 736   | 95.4 | 3.0 | 278  | 2 | BB173822 | BB173822 | BB173822  |
| 737   | 95.4 | 3.0 | 281  | 2 | BB108075 | BB108075 | BB108075  |
| 738   | 95.4 | 3.0 | 436  | 5 | BY487960 | BY487960 | BY487960  |
| 739   | 95.2 | 3.0 | 227  | 2 | BB501238 | BB501238 | BB501238  |
| 740   | 95.2 | 3.0 | 243  | 1 | AV232151 | AV232151 | AV232151  |
| 741   | 95.2 | 3.0 | 246  | 2 | BB301620 | BB301620 | BB301620  |
| 742   | 95.2 | 3.0 | 297  | 2 | BB135944 | BB135944 | BB135944  |
| 743   | 95.2 | 3.0 | 325  | 2 | BB218380 | BB218380 | BB218380  |
| c 744 | 95.2 | 3.0 | 434  | 4 | BM193462 | BM193462 | TCBAP1Q13 |
| 745   | 95.2 | 3.0 | 490  | 1 | AI365650 | AI365650 | ap20h08.x |
| 746   | 95   | 3.0 | 380  | 5 | BY165728 | BY165728 | BY165728  |
| 747   | 95   | 3.0 | 459  | 2 | BB633829 | BB633829 | BB633829  |
| 748   | 95   | 3.0 | 519  | 2 | BF046214 | BF046214 | BP250021A |
| 749   | 95   | 3.0 | 541  | 2 | BF045972 | BF045972 | BP250003B |

|   |     |      |     |      |   |          |          |           |
|---|-----|------|-----|------|---|----------|----------|-----------|
|   | 750 | 95   | 3.0 | 542  | 2 | BF039059 | BF039059 | BP250018B |
|   | 751 | 95   | 3.0 | 648  | 6 | CB419189 | CB419189 | 592037 MA |
|   | 752 | 94.8 | 3.0 | 336  | 2 | BB241589 | BB241589 | BB241589  |
|   | 753 | 94.8 | 3.0 | 710  | 6 | CA379066 | CA379066 | 658061 NC |
|   | 754 | 94.8 | 3.0 | 4045 | 3 | BC059007 | BC059007 | Mus muscu |
|   | 755 | 94.6 | 3.0 | 248  | 1 | AV326941 | AV326941 | AV326941  |
|   | 756 | 94.6 | 3.0 | 267  | 2 | BB108706 | BB108706 | BB108706  |
|   | 757 | 94.6 | 3.0 | 278  | 2 | BB479760 | BB479760 | BB479760  |
|   | 758 | 94.6 | 3.0 | 281  | 2 | BB221528 | BB221528 | BB221528  |
|   | 759 | 94.6 | 3.0 | 531  | 2 | BE235013 | BE235013 | 142239 MA |
|   | 760 | 94.6 | 3.0 | 703  | 5 | BM951868 | BM951868 | UI-M-EH0- |
|   | 761 | 94.4 | 3.0 | 275  | 2 | BB336194 | BB336194 | BB336194  |
|   | 762 | 94.4 | 3.0 | 291  | 1 | AV339535 | AV339535 | AV339535  |
|   | 763 | 94.4 | 3.0 | 336  | 2 | BB497526 | BB497526 | BB497526  |
|   | 764 | 94.4 | 3.0 | 520  | 7 | CN255484 | CN255484 | 170005313 |
|   | 765 | 94.4 | 3.0 | 954  | 4 | BG829919 | BG829919 | 602764325 |
|   | 766 | 94.2 | 3.0 | 211  | 2 | BB591302 | BB591302 | BB591302  |
|   | 767 | 94.2 | 3.0 | 481  | 7 | CK392759 | CK392759 | K0849F03- |
|   | 768 | 94.2 | 3.0 | 690  | 6 | BY734086 | BY734086 | BY734086  |
|   | 769 | 94.2 | 3.0 | 819  | 6 | CD628635 | CD628635 | 56097918H |
| c | 770 | 94.2 | 3.0 | 828  | 5 | BX665346 | BX665346 | BX665346  |
|   | 771 | 94   | 3.0 | 230  | 2 | BB254403 | BB254403 | BB254403  |
|   | 772 | 94   | 3.0 | 301  | 2 | BB335163 | BB335163 | BB335163  |
|   | 773 | 94   | 3.0 | 589  | 4 | BM150494 | BM150494 | TCBAP1D10 |
|   | 774 | 93.8 | 3.0 | 227  | 2 | BB213341 | BB213341 | BB213341  |
|   | 775 | 93.8 | 3.0 | 249  | 2 | BB324195 | BB324195 | BB324195  |
|   | 776 | 93.8 | 3.0 | 575  | 2 | BE245715 | BE245715 | TCBAP1D19 |
|   | 777 | 93.6 | 3.0 | 225  | 2 | BB270419 | BB270419 | BB270419  |
|   | 778 | 93.6 | 3.0 | 229  | 2 | BB217995 | BB217995 | BB217995  |
|   | 779 | 93.6 | 3.0 | 237  | 2 | BB431741 | BB431741 | BB431741  |
|   | 780 | 93.6 | 3.0 | 238  | 2 | BB356581 | BB356581 | BB356581  |
|   | 781 | 93.6 | 3.0 | 239  | 1 | AV238091 | AV238091 | AV238091  |
|   | 782 | 93.6 | 3.0 | 241  | 1 | AV341229 | AV341229 | AV341229  |
|   | 783 | 93.6 | 3.0 | 241  | 2 | BB073528 | BB073528 | BB073528  |
|   | 784 | 93.6 | 3.0 | 254  | 2 | BB258946 | BB258946 | BB258946  |
|   | 785 | 93.6 | 3.0 | 259  | 2 | BB215951 | BB215951 | BB215951  |
|   | 786 | 93.6 | 3.0 | 478  | 2 | BF654570 | BF654570 | 278796 MA |
|   | 787 | 93.4 | 3.0 | 244  | 2 | BB519336 | BB519336 | BB519336  |
|   | 788 | 93.2 | 3.0 | 146  | 4 | BI847990 | BI847990 | 470271 MA |
|   | 789 | 93.2 | 3.0 | 244  | 2 | BB242763 | BB242763 | BB242763  |
|   | 790 | 93.2 | 3.0 | 265  | 1 | AV286945 | AV286945 | AV286945  |
| c | 791 | 93.2 | 3.0 | 515  | 1 | AL928354 | AL928354 | AL928354  |
|   | 792 | 93.2 | 3.0 | 2340 | 9 | AY421319 | AY421319 | Mus muscu |
|   | 793 | 93.2 | 3.0 | 3159 | 3 | AK046502 | AK046502 | Mus muscu |
|   | 794 | 93.2 | 3.0 | 3225 | 9 | AY400493 | AY400493 | Mus muscu |
|   | 795 | 93.2 | 3.0 | 3726 | 3 | AK043386 | AK043386 | Mus muscu |
|   | 796 | 93   | 3.0 | 231  | 2 | BB151727 | BB151727 | BB151727  |
|   | 797 | 93   | 3.0 | 527  | 2 | BF462568 | BF462568 | UI-M-CG0p |
|   | 798 | 93   | 3.0 | 725  | 6 | CB520645 | CB520645 | UI-M-GI0- |
|   | 799 | 92.6 | 2.9 | 198  | 4 | BI021066 | BI021066 | PM3-MT020 |
|   | 800 | 92.6 | 2.9 | 228  | 2 | BB073945 | BB073945 | BB073945  |
|   | 801 | 92.6 | 2.9 | 289  | 2 | BB720615 | BB720615 | BB720615  |
|   | 802 | 92.6 | 2.9 | 377  | 5 | BY165251 | BY165251 | BY165251  |
|   | 803 | 92.6 | 2.9 | 546  | 6 | CA406911 | CA406911 | 1003060 H |
|   | 804 | 92.6 | 2.9 | 2575 | 3 | AK031231 | AK031231 | Mus muscu |
|   | 805 | 92.4 | 2.9 | 274  | 2 | BB177348 | BB177348 | BB177348  |
| c | 806 | 92.4 | 2.9 | 404  | 4 | BM174889 | BM174889 | hippo_08_ |

|       |      |     |     |   |          |          |           |
|-------|------|-----|-----|---|----------|----------|-----------|
| 807   | 92.2 | 2.9 | 587 | 5 | BP214222 | BP214222 | BP214222  |
| 808   | 92.2 | 2.9 | 691 | 5 | BM944530 | BM944530 | UI-M-EH0p |
| 809   | 92   | 2.9 | 239 | 2 | BB356352 | BB356352 | BB356352  |
| 810   | 92   | 2.9 | 274 | 2 | BB551851 | BB551851 | BB551851  |
| 811   | 92   | 2.9 | 343 | 2 | BB224139 | BB224139 | BB224139  |
| 812   | 92   | 2.9 | 492 | 7 | CN333872 | CN333872 | 170005325 |
| 813   | 92   | 2.9 | 518 | 2 | BF714462 | BF714462 | mab01a06. |
| 814   | 92   | 2.9 | 748 | 7 | CN333873 | CN333873 | 170006000 |
| 815   | 91.8 | 2.9 | 593 | 7 | CN255490 | CN255490 | 170006000 |
| 816   | 91.8 | 2.9 | 734 | 7 | CO395136 | CO395136 | AGENCOURT |
| 817   | 91.8 | 2.9 | 918 | 7 | CF780707 | CF780707 | AGENCOURT |
| 818   | 91.6 | 2.9 | 247 | 2 | BB170802 | BB170802 | BB170802  |
| c 819 | 91.6 | 2.9 | 434 | 1 | AV608925 | AV608925 | AV608925  |
| 820   | 91.6 | 2.9 | 704 | 6 | CB527136 | CB527136 | UI-M-FY0- |
| 821   | 91.6 | 2.9 | 937 | 5 | BU518484 | BU518484 | AGENCOURT |
| 822   | 91.4 | 2.9 | 433 | 6 | BY580507 | BY580507 | BY580507  |
| 823   | 91.4 | 2.9 | 600 | 5 | BU925145 | BU925145 | 7112-63 M |
| 824   | 91.2 | 2.9 | 281 | 6 | CD631369 | CD631369 | 56027863H |
| 825   | 91.2 | 2.9 | 543 | 6 | CD216128 | CD216128 | pgp2n.pk0 |
| 826   | 91.2 | 2.9 | 756 | 4 | BI645497 | BI645497 | 603275463 |
| 827   | 91   | 2.9 | 229 | 1 | AV232333 | AV232333 | AV232333  |
| 828   | 91   | 2.9 | 625 | 6 | CB247662 | CB247662 | UI-M-FI0- |
| 829   | 91   | 2.9 | 740 | 7 | CF532104 | CF532104 | UI-M-FY0- |
| c 830 | 90.8 | 2.9 | 228 | 6 | CB168395 | CB168395 | HSF603268 |
| 831   | 90.8 | 2.9 | 657 | 7 | CN788571 | CN788571 | 4122921 B |
| 832   | 90.6 | 2.9 | 283 | 1 | AV224722 | AV224722 | AV224722  |
| 833   | 90.6 | 2.9 | 827 | 4 | BF981141 | BF981141 | 602310407 |
| 834   | 90.4 | 2.9 | 230 | 2 | BB270171 | BB270171 | BB270171  |
| 835   | 90.4 | 2.9 | 239 | 2 | BB267673 | BB267673 | BB267673  |
| 836   | 90.4 | 2.9 | 369 | 5 | BY170960 | BY170960 | BY170960  |
| 837   | 90.2 | 2.9 | 238 | 2 | BB356191 | BB356191 | BB356191  |
| 838   | 89.8 | 2.9 | 235 | 2 | BB170781 | BB170781 | BB170781  |
| 839   | 89.8 | 2.9 | 245 | 2 | BB149370 | BB149370 | BB149370  |
| 840   | 89.8 | 2.9 | 896 | 4 | BI457032 | BI457032 | 603185949 |
| 841   | 89.6 | 2.9 | 279 | 2 | BB177200 | BB177200 | BB177200  |
| 842   | 89.4 | 2.8 | 256 | 7 | CN223998 | CN223998 | WLA052F08 |
| 843   | 89.4 | 2.8 | 574 | 5 | BM946983 | BM946983 | UI-M-EH0p |
| 844   | 89.2 | 2.8 | 329 | 2 | BB499916 | BB499916 | BB499916  |
| 845   | 89   | 2.8 | 231 | 2 | BB148551 | BB148551 | BB148551  |
| 846   | 89   | 2.8 | 255 | 2 | BB001987 | BB001987 | BB001987  |
| 847   | 89   | 2.8 | 456 | 5 | BY491040 | BY491040 | BY491040  |
| 848   | 89   | 2.8 | 509 | 2 | AW964929 | AW964929 | EST376897 |
| 849   | 88.8 | 2.8 | 228 | 2 | BB341090 | BB341090 | BB341090  |
| 850   | 88.8 | 2.8 | 232 | 2 | BB009287 | BB009287 | BB009287  |
| 851   | 88.6 | 2.8 | 593 | 5 | BP249762 | BP249762 | BP249762  |
| c 852 | 88.6 | 2.8 | 873 | 5 | BX770216 | BX770216 | BX770216  |
| 853   | 88.2 | 2.8 | 567 | 4 | BG710581 | BG710581 | pglln.pk0 |
| 854   | 88   | 2.8 | 282 | 2 | BB531669 | BB531669 | BB531669  |
| 855   | 88   | 2.8 | 745 | 6 | CA388534 | CA388534 | 670926 NC |
| 856   | 87.8 | 2.8 | 256 | 5 | BM948107 | BM948107 | UI-M-EG0p |
| 857   | 87.8 | 2.8 | 824 | 4 | BI161136 | BI161136 | 602865179 |
| 858   | 87.4 | 2.8 | 229 | 2 | BB173708 | BB173708 | BB173708  |
| 859   | 87.4 | 2.8 | 234 | 2 | BB717863 | BB717863 | BB717863  |
| 860   | 87.4 | 2.8 | 340 | 5 | BY207534 | BY207534 | BY207534  |
| 861   | 87.4 | 2.8 | 745 | 5 | BU055918 | BU055918 | UI-M-FO0- |
| 862   | 87.2 | 2.8 | 229 | 2 | BB239543 | BB239543 | BB239543  |
| 863   | 87.2 | 2.8 | 240 | 2 | BB326658 | BB326658 | BB326658  |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 864   | 87   | 2.8 | 697  | 2 | AW134401 | AW134401 | fi18h09.y |
| 865   | 87   | 2.8 | 770  | 6 | CD628629 | CD628629 | 56097478H |
| 866   | 86.8 | 2.8 | 242  | 2 | BB359459 | BB359459 | BB359459  |
| 867   | 86.8 | 2.8 | 258  | 1 | AV375018 | AV375018 | AV375018  |
| 868   | 86.6 | 2.8 | 433  | 5 | BY376940 | BY376940 | BY376940  |
| 869   | 86.6 | 2.8 | 917  | 2 | BE908445 | BE908445 | 601503077 |
| 870   | 86.6 | 2.8 | 923  | 4 | BI665624 | BI665624 | 603289613 |
| 871   | 86.6 | 2.8 | 2376 | 3 | AK045236 | AK045236 | Mus muscu |
| 872   | 86.4 | 2.7 | 216  | 2 | BB323957 | BB323957 | BB323957  |
| 873   | 86.4 | 2.7 | 462  | 6 | CD553207 | CD553207 | B0356E10- |
| 874   | 86.4 | 2.7 | 621  | 4 | BM738310 | BM738310 | K-EST0003 |
| 875   | 86.4 | 2.7 | 631  | 6 | BY724321 | BY724321 | BY724321  |
| 876   | 86.4 | 2.7 | 632  | 2 | BE270240 | BE270240 | 601186027 |
| c 877 | 86.4 | 2.7 | 646  | 2 | BF322402 | BF322402 | maa24f04. |
| 878   | 86.4 | 2.7 | 966  | 5 | BQ715428 | BQ715428 | AGENCOURT |
| 879   | 86.2 | 2.7 | 208  | 2 | BB079119 | BB079119 | BB079119  |
| 880   | 86.2 | 2.7 | 242  | 1 | AV381879 | AV381879 | AV381879  |
| 881   | 86.2 | 2.7 | 249  | 2 | BB215799 | BB215799 | BB215799  |
| 882   | 86.2 | 2.7 | 929  | 5 | BQ917819 | BQ917819 | AGENCOURT |
| 883   | 86   | 2.7 | 211  | 2 | BB184958 | BB184958 | BB184958  |
| 884   | 86   | 2.7 | 280  | 2 | BB142942 | BB142942 | BB142942  |
| 885   | 86   | 2.7 | 570  | 2 | BE407695 | BE407695 | 601299714 |
| 886   | 85.8 | 2.7 | 543  | 2 | AW966670 | AW966670 | EST378744 |
| 887   | 85.8 | 2.7 | 757  | 4 | BI735927 | BI735927 | 603360340 |
| 888   | 85.6 | 2.7 | 224  | 2 | BB171694 | BB171694 | BB171694  |
| 889   | 85.6 | 2.7 | 245  | 1 | AV232593 | AV232593 | AV232593  |
| 890   | 85.6 | 2.7 | 673  | 7 | CN401143 | CN401143 | 170005322 |
| 891   | 85.6 | 2.7 | 900  | 6 | CA321459 | CA321459 | UI-M-FW0- |
| 892   | 85.6 | 2.7 | 965  | 5 | BU845252 | BU845252 | AGENCOURT |
| 893   | 85.6 | 2.7 | 977  | 5 | BU855862 | BU855862 | AGENCOURT |
| 894   | 85.4 | 2.7 | 284  | 2 | BB181557 | BB181557 | BB181557  |
| 895   | 85.4 | 2.7 | 356  | 5 | BY204763 | BY204763 | BY204763  |
| 896   | 85.4 | 2.7 | 515  | 2 | BB633428 | BB633428 | BB633428  |
| 897   | 85.2 | 2.7 | 207  | 2 | BB214019 | BB214019 | BB214019  |
| 898   | 85.2 | 2.7 | 620  | 5 | BM943707 | BM943707 | UI-M-EH0p |
| 899   | 85   | 2.7 | 306  | 2 | BB030476 | BB030476 | BB030476  |
| 900   | 84.6 | 2.7 | 232  | 2 | BB262137 | BB262137 | BB262137  |
| 901   | 84.6 | 2.7 | 264  | 2 | BB534094 | BB534094 | BB534094  |
| 902   | 84.6 | 2.7 | 266  | 2 | BB196113 | BB196113 | BB196113  |
| 903   | 84.6 | 2.7 | 698  | 5 | BU227771 | BU227771 | 603800481 |
| 904   | 84.4 | 2.7 | 628  | 6 | CA318117 | CA318117 | UI-M-FW0- |
| 905   | 84.4 | 2.7 | 1010 | 5 | BX360753 | BX360753 | BX360753  |
| 906   | 84.4 | 2.7 | 1246 | 2 | BF166143 | BF166143 | 601776590 |
| 907   | 84.2 | 2.7 | 218  | 2 | BB213301 | BB213301 | BB213301  |
| 908   | 84   | 2.7 | 456  | 5 | BY155480 | BY155480 | BY155480  |
| 909   | 84   | 2.7 | 790  | 6 | CB248961 | CB248961 | UI-M-EX0- |
| 910   | 84   | 2.7 | 864  | 5 | BU156223 | BU156223 | AGENCOURT |
| 911   | 83.8 | 2.7 | 214  | 2 | BB588963 | BB588963 | BB588963  |
| 912   | 83.6 | 2.7 | 249  | 1 | AV381817 | AV381817 | AV381817  |
| 913   | 83.4 | 2.7 | 270  | 2 | BB177951 | BB177951 | BB177951  |
| 914   | 83.4 | 2.7 | 720  | 6 | CD628637 | CD628637 | 56098002H |
| 915   | 83.4 | 2.7 | 777  | 6 | CB248692 | CB248692 | UI-M-EX0- |
| 916   | 83   | 2.6 | 227  | 2 | BB216867 | BB216867 | BB216867  |
| c 917 | 83   | 2.6 | 338  | 6 | CB060198 | CB060198 | 4010590 B |
| 918   | 83   | 2.6 | 691  | 5 | BQ180084 | BQ180084 | UI-M-EW0- |
| 919   | 82.8 | 2.6 | 334  | 5 | BY023564 | BY023564 | BY023564  |
| 920   | 82.8 | 2.6 | 425  | 1 | AV665430 | AV665430 | AV665430  |

|   |     |      |     |      |   |          |          |           |     |
|---|-----|------|-----|------|---|----------|----------|-----------|-----|
|   | 921 | 82.8 | 2.6 | 511  | 6 | CA383610 | CA383610 | 663812    | NC  |
|   | 922 | 82.8 | 2.6 | 647  | 5 | BM950623 | BM950623 | UI-M-EH0p |     |
|   | 923 | 82.6 | 2.6 | 410  | 5 | BU428839 | BU428839 | UI-HF-BN0 |     |
|   | 924 | 82.6 | 2.6 | 445  | 2 | BE244550 | BE244550 | TCBAP1D11 |     |
|   | 925 | 82.6 | 2.6 | 492  | 2 | BE018639 | BE018639 | bb83a12.y |     |
|   | 926 | 82.6 | 2.6 | 549  | 2 | AW655369 | AW655369 | 106098    | MA  |
|   | 927 | 82.6 | 2.6 | 638  | 2 | AW245910 | AW245910 | 2822888.5 |     |
| c | 928 | 82.4 | 2.6 | 139  | 7 | CK942460 | CK942460 | 4066200   | B   |
|   | 929 | 82.4 | 2.6 | 227  | 2 | BB221591 | BB221591 | BB221591  |     |
|   | 930 | 82.4 | 2.6 | 569  | 2 | AW499893 | AW499893 | UI-HF-BN0 |     |
|   | 931 | 82.4 | 2.6 | 582  | 5 | BP348794 | BP348794 | BP348794  |     |
|   | 932 | 82   | 2.6 | 200  | 6 | BY589580 | BY589580 | BY589580  |     |
|   | 933 | 82   | 2.6 | 224  | 2 | BB170950 | BB170950 | BB170950  |     |
|   | 934 | 82   | 2.6 | 314  | 5 | BY347200 | BY347200 | BY347200  |     |
|   | 935 | 82   | 2.6 | 855  | 5 | BQ770087 | BQ770087 | UI-M-FI0- |     |
|   | 936 | 81.8 | 2.6 | 228  | 1 | AV231620 | AV231620 | AV231620  |     |
| c | 937 | 81.6 | 2.6 | 377  | 2 | BE246473 | BE246473 | TCBAP1E47 |     |
|   | 938 | 81.4 | 2.6 | 2292 | 9 | AY402638 | AY402638 | Mus muscu |     |
|   | 939 | 81.2 | 2.6 | 707  | 6 | BY733150 | BY733150 | BY733150  |     |
|   | 940 | 81.2 | 2.6 | 821  | 7 | CK846765 | CK846765 | 969310    | MA  |
|   | 941 | 81   | 2.6 | 553  | 7 | CN684594 | CN684594 | E0195H06- |     |
|   | 942 | 80.8 | 2.6 | 378  | 2 | BB745658 | BB745658 | BB745658  |     |
|   | 943 | 80.8 | 2.6 | 459  | 4 | BJ043336 | BJ043336 | BJ043336  |     |
|   | 944 | 80.8 | 2.6 | 479  | 2 | BF731124 | BF731124 | mab81e06. |     |
|   | 945 | 80.4 | 2.6 | 240  | 2 | BB301102 | BB301102 | BB301102  |     |
|   | 946 | 80.4 | 2.6 | 405  | 6 | CB808856 | CB808856 | AMGNNUC:S |     |
|   | 947 | 80.4 | 2.6 | 625  | 6 | CD348364 | CD348364 | UI-M-FY0- |     |
| c | 948 | 80.4 | 2.6 | 763  | 6 | CD619057 | CD619057 | 56030577H |     |
|   | 949 | 80.4 | 2.6 | 785  | 4 | BI194687 | BI194687 | 602946246 |     |
|   | 950 | 80.4 | 2.6 | 797  | 7 | CO404183 | CO404183 | AGENCOURT |     |
|   | 951 | 80.4 | 2.6 | 890  | 5 | BU856543 | BU856543 | AGENCOURT |     |
|   | 952 | 80.2 | 2.6 | 363  | 5 | BY344602 | BY344602 | BY344602  |     |
|   | 953 | 80.2 | 2.6 | 850  | 5 | BM944264 | BM944264 | UI-M-EH0p |     |
|   | 954 | 80.2 | 2.6 | 900  | 7 | CK799299 | CK799299 | AGENCOURT |     |
| c | 955 | 79.8 | 2.5 | 307  | 4 | BF961259 | BF961259 | PM1-NN120 |     |
|   | 956 | 79.8 | 2.5 | 700  | 6 | CD628633 | CD628633 | 56097902H |     |
|   | 957 | 79.6 | 2.5 | 233  | 2 | BB134411 | BB134411 | BB134411  |     |
|   | 958 | 79.6 | 2.5 | 237  | 2 | BB593564 | BB593564 | BB593564  |     |
|   | 959 | 79.6 | 2.5 | 268  | 2 | BB383954 | BB383954 | BB383954  |     |
| c | 960 | 79.6 | 2.5 | 426  | 4 | BF954455 | BF954455 | MR4-NN020 |     |
|   | 961 | 79.6 | 2.5 | 718  | 4 | BG475468 | BG475468 | 602491461 |     |
|   | 962 | 79.6 | 2.5 | 801  | 5 | BX313585 | BX313585 | BX313585  |     |
|   | 963 | 79.6 | 2.5 | 922  | 5 | BQ943695 | BQ943695 | AGENCOURT |     |
|   | 964 | 79.6 | 2.5 | 2349 | 9 | AY421317 | AY421317 | Homo sapi |     |
|   | 965 | 79.4 | 2.5 | 581  | 5 | BX310430 | BX310430 | BX310430  |     |
|   | 966 | 79.4 | 2.5 | 643  | 5 | BX087763 | BX087763 | BX087763  |     |
|   | 967 | 79.2 | 2.5 | 362  | 5 | BY344235 | BY344235 | BY344235  |     |
| c | 968 | 79.2 | 2.5 | 457  | 2 | AW462107 | AW462107 | BP230008A |     |
|   | 969 | 79.2 | 2.5 | 647  | 2 | BE907509 | BE907509 | 601497468 |     |
|   | 970 | 79   | 2.5 | 295  | 2 | BB354856 | BB354856 | BB354856  |     |
|   | 971 | 79   | 2.5 | 453  | 2 | AW500044 | AW500044 | UI-HF-BN0 |     |
|   | 972 | 79   | 2.5 | 593  | 5 | BQ266902 | BQ266902 | NISC_ff15 |     |
|   | 973 | 79   | 2.5 | 978  | 5 | BQ963608 | BQ963608 | AGENCOURT |     |
|   | 974 | 78.8 | 2.5 | 696  | 7 | CK974651 | CK974651 | 4105581   | B   |
|   | 975 | 78.8 | 2.5 | 826  | 6 | CD628641 | CD628641 | 56097486H |     |
|   | 976 | 78.6 | 2.5 | 474  | 2 | AW659439 | AW659439 | 96609     | MAR |
| c | 977 | 78.6 | 2.5 | 599  | 2 | BF357811 | BF357811 | RC2-LT000 |     |



|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 978   | 78.4 | 2.5 | 450  | 2 | BE653346 | BE653346 | UI-M-AL1- |
| 979   | 78.4 | 2.5 | 490  | 6 | CA531840 | CA531840 | C0325D06- |
| 980   | 78.4 | 2.5 | 645  | 7 | CF170234 | CF170234 | B0824E08- |
| 981   | 78.4 | 2.5 | 696  | 7 | CF168782 | CF168782 | B0804F02- |
| 982   | 78.4 | 2.5 | 719  | 7 | CK636248 | CK636248 | UI-M-HN0- |
| 983   | 78.2 | 2.5 | 225  | 2 | BB443283 | BB443283 | BB443283  |
| 984   | 78.2 | 2.5 | 231  | 2 | BB148230 | BB148230 | BB148230  |
| c 985 | 78.2 | 2.5 | 254  | 6 | CB469624 | CB469624 | sn09_H09. |
| 986   | 78   | 2.5 | 239  | 2 | BB109818 | BB109818 | BB109818  |
| 987   | 77.8 | 2.5 | 219  | 1 | AV369146 | AV369146 | AV369146  |
| c 988 | 77.8 | 2.5 | 551  | 2 | BF516420 | BF516420 | UI-H-BW1- |
| 989   | 77.6 | 2.5 | 175  | 1 | AV375624 | AV375624 | AV375624  |
| 990   | 77.2 | 2.5 | 887  | 5 | BU906435 | BU906435 | AGENCOURT |
| c 991 | 77   | 2.4 | 703  | 5 | BM936326 | BM936326 | UI-M-CG0p |
| 992   | 76.8 | 2.4 | 438  | 7 | CF535009 | CF535009 | UI-M-GH0- |
| 993   | 76.8 | 2.4 | 687  | 4 | BG327618 | BG327618 | 602426612 |
| 994   | 76.6 | 2.4 | 357  | 1 | AI877089 | AI877089 | vz73g04.r |
| 995   | 76.6 | 2.4 | 443  | 4 | BM484413 | BM484413 | 538266 MA |
| 996   | 76.6 | 2.4 | 469  | 7 | CN429211 | CN429211 | 170005327 |
| 997   | 76.6 | 2.4 | 862  | 1 | AU118557 | AU118557 | AU118557  |
| c 998 | 76.4 | 2.4 | 106  | 6 | CD631365 | CD631365 | 56027747H |
| 999   | 76.2 | 2.4 | 234  | 1 | AV250428 | AV250428 | AV250428  |
| 1000  | 76.2 | 2.4 | 904  | 5 | BU145486 | BU145486 | AGENCOURT |
| 1001  | 76.2 | 2.4 | 2224 | 9 | AY421318 | AY421318 | Pan trogl |
| 1002  | 76   | 2.4 | 77   | 6 | CD631368 | CD631368 | 56027839J |
| 1003  | 76   | 2.4 | 223  | 2 | BB330942 | BB330942 | BB330942  |
| 1004  | 76   | 2.4 | 283  | 6 | CD631364 | CD631364 | 56027739J |
| 1005  | 76   | 2.4 | 600  | 4 | BI986000 | BI986000 | 3154-38 M |
| 1006  | 75.8 | 2.4 | 225  | 2 | BB214723 | BB214723 | BB214723  |
| 1007  | 75.8 | 2.4 | 699  | 6 | CD628631 | CD628631 | 56097494H |
| 1008  | 75.2 | 2.4 | 234  | 2 | BB327897 | BB327897 | BB327897  |
| 1009  | 75.2 | 2.4 | 464  | 2 | BE263633 | BE263633 | 601192057 |
| 1010  | 75.2 | 2.4 | 658  | 4 | BG424478 | BG424478 | 602447602 |
| 1011  | 75.2 | 2.4 | 715  | 5 | BX849809 | BX849809 | BX849809  |
| 1012  | 75.2 | 2.4 | 865  | 5 | BX844237 | BX844237 | BX844237  |
| 1013  | 75.2 | 2.4 | 917  | 5 | BQ224963 | BQ224963 | AGENCOURT |
| 1014  | 75   | 2.4 | 158  | 2 | BB244145 | BB244145 | BB244145  |
| 1015  | 75   | 2.4 | 622  | 6 | CA324358 | CA324358 | UI-M-FY0- |
| 1016  | 75   | 2.4 | 1129 | 5 | BQ071719 | BQ071719 | AGENCOURT |
| c1017 | 74.8 | 2.4 | 462  | 4 | BF944916 | BF944916 | CM1-NN019 |
| c1018 | 74.6 | 2.4 | 130  | 2 | BE349795 | BE349795 | hq43b12.x |
| 1019  | 74.6 | 2.4 | 789  | 4 | BI686539 | BI686539 | 603313631 |
| c1020 | 74.4 | 2.4 | 228  | 1 | AI323583 | AI323583 | mp57e06.x |
| 1021  | 74.4 | 2.4 | 467  | 2 | BF443467 | BF443467 | 260957 MA |
| 1022  | 74.4 | 2.4 | 661  | 7 | CN333878 | CN333878 | 170005315 |
| 1023  | 74.4 | 2.4 | 748  | 7 | CF747865 | CF747865 | UI-M-HE0- |
| 1024  | 74.4 | 2.4 | 763  | 7 | CN461035 | CN461035 | UI-M-HB0- |
| 1025  | 74   | 2.4 | 410  | 2 | AW477508 | AW477508 | 12794 MAR |
| 1026  | 74   | 2.4 | 725  | 7 | CN429210 | CN429210 | 170004241 |
| 1027  | 74   | 2.4 | 771  | 7 | CF285178 | CF285178 | AGENCOURT |
| 1028  | 73.8 | 2.3 | 182  | 2 | BB083305 | BB083305 | BB083305  |
| 1029  | 73.8 | 2.3 | 228  | 1 | AV173854 | AV173854 | AV173854  |
| 1030  | 73.8 | 2.3 | 989  | 6 | CA454865 | CA454865 | AGENCOURT |
| 1031  | 73.6 | 2.3 | 414  | 6 | CB801298 | CB801298 | AMGNNUC:M |
| 1032  | 73.4 | 2.3 | 184  | 2 | BB216676 | BB216676 | BB216676  |
| 1033  | 73.4 | 2.3 | 878  | 4 | BM042998 | BM042998 | 603619122 |
| 1034  | 73.4 | 2.3 | 1019 | 1 | AL541401 | AL541401 | AL541401  |

|       |      |     |      |   |          |          |             |
|-------|------|-----|------|---|----------|----------|-------------|
| 1035  | 73.2 | 2.3 | 154  | 1 | AV230195 | AV230195 | AV230195    |
| 1036  | 73.2 | 2.3 | 430  | 6 | CB760771 | CB760771 | AMGNNUC:T   |
| 1037  | 73.2 | 2.3 | 580  | 7 | CN333883 | CN333883 | 170005318   |
| 1038  | 73   | 2.3 | 275  | 2 | BB604391 | BB604391 | BB604391    |
| c1039 | 73   | 2.3 | 526  | 5 | BX267431 | BX267431 | BX267431    |
| c1040 | 73   | 2.3 | 526  | 5 | BX270851 | BX270851 | BX270851    |
| c1041 | 73   | 2.3 | 528  | 5 | BX270850 | BX270850 | BX270850    |
| 1042  | 73   | 2.3 | 716  | 7 | CF747885 | CF747885 | UI-M-HE0-   |
| 1043  | 73   | 2.3 | 851  | 6 | CD653925 | CD653925 | AGENCOURT   |
| c1044 | 73   | 2.3 | 963  | 9 | CC841964 | CC841964 | NDL.130G1   |
| 1045  | 73   | 2.3 | 3225 | 9 | AY400492 | AY400492 | Pan trogl   |
| c1046 | 72.8 | 2.3 | 355  | 6 | CD631361 | CD631361 | 56027755H   |
| 1047  | 72.8 | 2.3 | 569  | 6 | CA352454 | CA352454 | 623718 NC   |
| 1048  | 72.6 | 2.3 | 636  | 5 | BQ109297 | BQ109297 | imageqc_6   |
| c1049 | 72.6 | 2.3 | 820  | 1 | AI800602 | AI800602 | wg12d10.x   |
| 1050  | 72.2 | 2.3 | 488  | 5 | BQ044885 | BQ044885 | UI-M-EH0p   |
| 1051  | 72.2 | 2.3 | 539  | 7 | CO051028 | CO051028 | Le_mx0_22   |
| 1052  | 72.2 | 2.3 | 843  | 7 | CF995086 | CF995086 | AGENCOURT   |
| 1053  | 72.2 | 2.3 | 914  | 6 | CA792253 | CA792253 | AGENCOURT   |
| 1054  | 71.8 | 2.3 | 228  | 2 | BB213582 | BB213582 | BB213582    |
| 1055  | 71.4 | 2.3 | 680  | 6 | BY735266 | BY735266 | BY735266    |
| 1056  | 71.4 | 2.3 | 715  | 6 | CD628625 | CD628625 | 56097386H   |
| 1057  | 71.4 | 2.3 | 3225 | 9 | AY400491 | AY400491 | Homo sapi   |
| 1058  | 71.2 | 2.3 | 381  | 6 | CB809999 | CB809999 | AMGNNUC:N   |
| c1059 | 71.2 | 2.3 | 396  | 2 | BE245837 | BE245837 | TCBAP1E19   |
| 1060  | 71.2 | 2.3 | 436  | 6 | BY536630 | BY536630 | BY536630    |
| 1061  | 71.2 | 2.3 | 1005 | 5 | BU553834 | BU553834 | AGENCOURT   |
| 1062  | 70.8 | 2.3 | 169  | 7 | CK377833 | CK377833 | lai09b12.   |
| 1063  | 70.8 | 2.3 | 188  | 1 | AV230685 | AV230685 | AV230685    |
| 1064  | 70.8 | 2.3 | 277  | 2 | BB529518 | BB529518 | BB529518    |
| 1065  | 70.8 | 2.3 | 805  | 6 | CD656935 | CD656935 | AGENCOURT   |
| 1066  | 70.6 | 2.2 | 767  | 9 | CL640550 | CL640550 | G076F10 G   |
| c1067 | 70.2 | 2.2 | 151  | 6 | CB475278 | CB475278 | jns105_D0   |
| 1068  | 70.2 | 2.2 | 390  | 9 | CL640447 | CL640447 | G074G07 G   |
| c1069 | 70   | 2.2 | 228  | 1 | AI837906 | AI837906 | UI-M-AL0-   |
| 1070  | 70   | 2.2 | 604  | 2 | BE283742 | BE283742 | 601103987   |
| 1071  | 70   | 2.2 | 777  | 7 | CK479930 | CK479930 | AGENCOURT   |
| 1072  | 70   | 2.2 | 1911 | 9 | AY403380 | AY403380 | Homo sapi   |
| 1073  | 69.8 | 2.2 | 163  | 7 | CF424452 | CF424452 | lad30g10.   |
| c1074 | 69.8 | 2.2 | 285  | 2 | BF874390 | BF874390 | QV2-ET010   |
| 1075  | 69.6 | 2.2 | 157  | 2 | BB151796 | BB151796 | BB151796    |
| 1076  | 69.6 | 2.2 | 266  | 7 | Z28925   | Z28925   | HSBC1H081 S |
| 1077  | 69.6 | 2.2 | 765  | 4 | BI823626 | BI823626 | 603038515   |
| 1078  | 69.6 | 2.2 | 832  | 7 | CN534073 | CN534073 | UI-M-HO0-   |
| 1079  | 69.6 | 2.2 | 1154 | 4 | BM462308 | BM462308 | AGENCOURT   |
| 1080  | 69.4 | 2.2 | 701  | 4 | BI194321 | BI194321 | 602947742   |
| 1081  | 69.2 | 2.2 | 343  | 5 | BY173287 | BY173287 | BY173287    |
| 1082  | 69.2 | 2.2 | 555  | 1 | AI641288 | AI641288 | fc13a11.y   |
| 1083  | 69   | 2.2 | 866  | 4 | BG923853 | BG923853 | 602824656   |
| 1084  | 69   | 2.2 | 894  | 4 | BG422248 | BG422248 | 602446883   |
| 1085  | 68.8 | 2.2 | 638  | 6 | CD215884 | CD215884 | pgp2n.pk0   |
| 1086  | 68.8 | 2.2 | 641  | 7 | CN665211 | CN665211 | A0823B11-   |
| 1087  | 68.8 | 2.2 | 728  | 6 | CD628623 | CD628623 | 56097378H   |
| 1088  | 68.6 | 2.2 | 695  | 5 | BQ769222 | BQ769222 | UI-M-FC0-   |
| c1089 | 68.4 | 2.2 | 325  | 2 | BE246184 | BE246184 | TCBAP2E06   |
| 1090  | 68.4 | 2.2 | 518  | 6 | BY593368 | BY593368 | BY593368    |
| 1091  | 68.2 | 2.2 | 439  | 1 | AA263826 | AA263826 | LD07023.5   |

|       |      |     |      |   |          |          |             |
|-------|------|-----|------|---|----------|----------|-------------|
| 1092  | 68   | 2.2 | 786  | 1 | AL584324 | AL584324 | AL584324    |
| 1093  | 67.8 | 2.2 | 243  | 7 | CO187281 | CO187281 | EK027722.   |
| 1094  | 67.8 | 2.2 | 591  | 1 | AL711630 | AL711630 | DKFZp686N   |
| 1095  | 67.8 | 2.2 | 626  | 7 | CF535272 | CF535272 | UI-M-GH0-   |
| 1096  | 67.8 | 2.2 | 689  | 7 | CN460658 | CN460658 | UI-M-HB0-   |
| 1097  | 67.8 | 2.2 | 849  | 7 | CF726328 | CF726328 | UI-M-HB0-   |
| 1098  | 67.6 | 2.2 | 177  | 2 | BB262424 | BB262424 | BB262424    |
| 1099  | 67.6 | 2.2 | 200  | 2 | BB213365 | BB213365 | BB213365    |
| 1100  | 67.6 | 2.2 | 562  | 4 | BM090629 | BM090629 | ig16e01.y   |
| 1101  | 67.6 | 2.2 | 582  | 5 | BP215174 | BP215174 | BP215174    |
| 1102  | 67.6 | 2.2 | 768  | 6 | CD619058 | CD619058 | 56030577J   |
| 1103  | 67.6 | 2.2 | 4847 | 3 | BC083186 | BC083186 | Mus muscu   |
| 1104  | 67.2 | 2.1 | 238  | 2 | BB593587 | BB593587 | BB593587    |
| 1105  | 67.2 | 2.1 | 394  | 6 | CB547006 | CB547006 | AMGNNUC:S   |
| 1106  | 67.2 | 2.1 | 692  | 7 | CN236752 | CN236752 | RJB124H02   |
| 1107  | 67.2 | 2.1 | 3394 | 3 | AK053632 | AK053632 | Mus muscu   |
| 1108  | 67   | 2.1 | 170  | 2 | BB218573 | BB218573 | BB218573    |
| 1109  | 66.8 | 2.1 | 639  | 7 | CV022901 | CV022901 | 340 Full    |
| c1110 | 66.8 | 2.1 | 710  | 1 | AI638881 | AI638881 | tt08d08.x   |
| 1111  | 66.8 | 2.1 | 967  | 5 | BX460723 | BX460723 | BX460723    |
| 1112  | 66.6 | 2.1 | 185  | 2 | BB008412 | BB008412 | BB008412    |
| 1113  | 66.6 | 2.1 | 291  | 6 | CB710224 | CB710224 | AMGNNUC:N   |
| 1114  | 66.6 | 2.1 | 813  | 6 | CA320357 | CA320357 | UI-M-FW0-   |
| 1115  | 66.4 | 2.1 | 656  | 7 | CF728356 | CF728356 | UI-M-HB0-   |
| 1116  | 66.4 | 2.1 | 777  | 7 | CF742166 | CF742166 | UI-M-HB0-   |
| 1117  | 66.4 | 2.1 | 813  | 2 | BE872958 | BE872958 | 601451552   |
| c1118 | 66.2 | 2.1 | 197  | 2 | AW048928 | AW048928 | UI-M-BH1-   |
| 1119  | 66   | 2.1 | 639  | 6 | CD502318 | CD502318 | CDA56-A04   |
| 1120  | 66   | 2.1 | 801  | 7 | CK679212 | CK679212 | ZF101-P00   |
| 1121  | 65.6 | 2.1 | 668  | 7 | CK836913 | CK836913 | 4062174 B   |
| 1122  | 65.6 | 2.1 | 690  | 4 | BG333712 | BG333712 | 602460715   |
| 1123  | 65.4 | 2.1 | 264  | 2 | BB532400 | BB532400 | BB532400    |
| 1124  | 65.4 | 2.1 | 580  | 5 | BP326398 | BP326398 | BP326398    |
| 1125  | 65.2 | 2.1 | 343  | 5 | BY351503 | BY351503 | BY351503    |
| 1126  | 65.2 | 2.1 | 731  | 7 | CN458596 | CN458596 | UI-M-HB0-   |
| 1127  | 65.2 | 2.1 | 834  | 7 | CF740100 | CF740100 | UI-M-HD0-   |
| 1128  | 65.2 | 2.1 | 1372 | 3 | AK039355 | AK039355 | Mus muscu   |
| 1129  | 65   | 2.1 | 497  | 6 | CA319520 | CA319520 | UI-M-FW0-   |
| 1130  | 65   | 2.1 | 701  | 6 | BY736064 | BY736064 | BY736064    |
| 1131  | 64.8 | 2.1 | 278  | 2 | BB523398 | BB523398 | BB523398    |
| 1132  | 64.8 | 2.1 | 597  | 7 | CN255479 | CN255479 | 170005322   |
| 1133  | 64.8 | 2.1 | 771  | 7 | CK791448 | CK791448 | AGENCOURT   |
| 1134  | 64.6 | 2.1 | 320  | 5 | BY346988 | BY346988 | BY346988    |
| 1135  | 64.2 | 2.0 | 346  | 5 | BY018991 | BY018991 | BY018991    |
| 1136  | 64   | 2.0 | 147  | 1 | AV315332 | AV315332 | AV315332    |
| 1137  | 64   | 2.0 | 576  | 7 | CN333867 | CN333867 | 170005318   |
| 1138  | 64   | 2.0 | 725  | 7 | CN457302 | CN457302 | UI-M-HN0-   |
| 1139  | 64   | 2.0 | 757  | 7 | CK635851 | CK635851 | UI-M-HN0-   |
| 1140  | 64   | 2.0 | 942  | 1 | AU078986 | AU078986 | AU078986    |
| 1141  | 64   | 2.0 | 976  | 9 | CNS02YCR | AL219492 | Tetraodon   |
| 1142  | 64   | 2.0 | 1155 | 2 | BF531775 | BF531775 | 602072681   |
| 1143  | 63.8 | 2.0 | 591  | 4 | BJ074142 | BJ074142 | BJ074142    |
| 1144  | 63.8 | 2.0 | 655  | 4 | BJ063284 | BJ063284 | BJ063284    |
| 1145  | 63.8 | 2.0 | 723  | 4 | BI870437 | BI870437 | 603395690   |
| 1146  | 63.8 | 2.0 | 900  | 6 | C82295   | C82295   | C82295 Leuk |
| 1147  | 63.8 | 2.0 | 2319 | 9 | AY402636 | AY402636 | Homo sapi   |
| 1148  | 63.8 | 2.0 | 2960 | 3 | AK043634 | AK043634 | Mus muscu   |

|       |      |     |      |   |          |          |             |
|-------|------|-----|------|---|----------|----------|-------------|
| 1149  | 63.8 | 2.0 | 3154 | 3 | AK033597 | AK033597 | Mus muscu   |
| 1150  | 63.8 | 2.0 | 3287 | 3 | AK048364 | AK048364 | Mus muscu   |
| 1151  | 63.8 | 2.0 | 3292 | 3 | AK037034 | AK037034 | Mus muscu   |
| 1152  | 63.8 | 2.0 | 3436 | 3 | AK014333 | AK014333 | Mus muscu   |
| 1153  | 63.6 | 2.0 | 233  | 2 | BB327844 | BB327844 | BB327844    |
| 1154  | 63.6 | 2.0 | 573  | 6 | CD214656 | CD214656 | pgm2n.pk0   |
| 1155  | 63.6 | 2.0 | 831  | 7 | CO433634 | CO433634 | UI-M-HX0-   |
| 1156  | 63.4 | 2.0 | 571  | 7 | CN401141 | CN401141 | 170006000   |
| 1157  | 63.4 | 2.0 | 676  | 6 | CD803405 | CD803405 | UI-M-GV0-   |
| 1158  | 63.4 | 2.0 | 889  | 1 | AU050267 | AU050267 | AU050267    |
| 1159  | 63.2 | 2.0 | 700  | 4 | BI143486 | BI143486 | 602907665   |
| 1160  | 63   | 2.0 | 232  | 2 | BB169302 | BB169302 | BB169302    |
| 1161  | 63   | 2.0 | 370  | 5 | BY028015 | BY028015 | BY028015    |
| 1162  | 62.8 | 2.0 | 1020 | 6 | CB590629 | CB590629 | AGENCOURT   |
| 1163  | 62.6 | 2.0 | 214  | 2 | BB269367 | BB269367 | BB269367    |
| c1164 | 62.6 | 2.0 | 384  | 2 | AW900477 | AW900477 | CM0-NN100   |
| 1165  | 62.6 | 2.0 | 469  | 7 | CN429155 | CN429155 | 170005318   |
| 1166  | 62.6 | 2.0 | 508  | 6 | CD675182 | CD675182 | fs20a08.y   |
| 1167  | 62.6 | 2.0 | 602  | 5 | BQ749127 | BQ749127 | UI-M-FD0-   |
| 1168  | 62.6 | 2.0 | 939  | 5 | BU915658 | BU915658 | AGENCOURT   |
| 1169  | 62.4 | 2.0 | 150  | 1 | AV237564 | AV237564 | AV237564    |
| 1170  | 62.4 | 2.0 | 555  | 7 | CN670016 | CN670016 | A0887D08-   |
| 1171  | 62.4 | 2.0 | 2289 | 9 | AY402637 | AY402637 | Pan trogl   |
| 1172  | 62.2 | 2.0 | 178  | 2 | BB603730 | BB603730 | BB603730    |
| 1173  | 62.2 | 2.0 | 857  | 4 | BI161471 | BI161471 | 602865054   |
| 1174  | 62   | 2.0 | 857  | 2 | BF580228 | BF580228 | 602099043   |
| 1175  | 62   | 2.0 | 883  | 5 | BU224821 | BU224821 | 603948128   |
| 1176  | 61.8 | 2.0 | 469  | 1 | AU279333 | AU279333 | AU279333    |
| 1177  | 61.8 | 2.0 | 685  | 1 | AL637843 | AL637843 | AL637843    |
| 1178  | 61.8 | 2.0 | 856  | 7 | CO246694 | CO246694 | AGENCOURT   |
| 1179  | 61.6 | 2.0 | 212  | 2 | BB587253 | BB587253 | BB587253    |
| c1180 | 61.6 | 2.0 | 580  | 7 | CO302404 | CO302404 | EK184063.   |
| 1181  | 61.6 | 2.0 | 859  | 5 | BQ571689 | BQ571689 | UI-M-FC0-   |
| 1182  | 61.4 | 2.0 | 155  | 2 | BB222407 | BB222407 | BB222407    |
| c1183 | 61.4 | 2.0 | 1056 | 9 | CNS00JQN | AL076816 | Drosophil   |
| 1184  | 61.2 | 1.9 | 170  | 2 | BB113286 | BB113286 | BB113286    |
| 1185  | 61.2 | 1.9 | 490  | 7 | CN538039 | CN538039 | UI-M-HS0-   |
| 1186  | 61.2 | 1.9 | 1084 | 4 | BG479750 | BG479750 | 602526948   |
| 1187  | 61   | 1.9 | 203  | 1 | AA326134 | AA326134 | EST29247    |
| c1188 | 61   | 1.9 | 398  | 1 | AI787249 | AI787249 | uj58a10.x   |
| 1189  | 61   | 1.9 | 421  | 7 | CN401145 | CN401145 | 170004241   |
| 1190  | 60.8 | 1.9 | 441  | 6 | CA871124 | CA871124 | K0908A03-   |
| 1191  | 60.8 | 1.9 | 1039 | 5 | BX458912 | BX458912 | BX458912    |
| 1192  | 60.8 | 1.9 | 1170 | 2 | BF345508 | BF345508 | 602019266   |
| 1193  | 60.6 | 1.9 | 207  | 7 | CN700205 | CN700205 | E0431G12-   |
| 1194  | 60.6 | 1.9 | 675  | 6 | BY718955 | BY718955 | BY718955    |
| 1195  | 60.6 | 1.9 | 959  | 1 | AL551337 | AL551337 | AL551337    |
| c1196 | 60   | 1.9 | 395  | 4 | BF947978 | BF947978 | CM1-NN019   |
| c1197 | 60   | 1.9 | 587  | 6 | CB585337 | CB585337 | AMGNNUC:U   |
| 1198  | 59.8 | 1.9 | 812  | 6 | CA317902 | CA317902 | UI-M-FW0-   |
| 1199  | 59.6 | 1.9 | 403  | 7 | CF535184 | CF535184 | UI-M-GI0-   |
| 1200  | 59.6 | 1.9 | 765  | 7 | CK366996 | CK366996 | AGENCOURT   |
| 1201  | 59.4 | 1.9 | 546  | 2 | BF194361 | BF194361 | 246370 MA   |
| 1202  | 59.4 | 1.9 | 736  | 5 | BM947302 | BM947302 | UI-M-EH0p   |
| 1203  | 59.2 | 1.9 | 986  | 4 | BI686422 | BI686422 | 603315567   |
| 1204  | 59   | 1.9 | 265  | 7 | M78717   | M78717   | EST00865 Hi |
| c1205 | 59   | 1.9 | 373  | 4 | BG998374 | BG998374 | PM4-HT130   |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 1206  | 59   | 1.9 | 983  | 5 | BQ879085 | BQ879085 | AGENCOURT |
| 1207  | 59   | 1.9 | 2227 | 9 | AY403445 | AY403445 | Mus muscu |
| 1208  | 58.8 | 1.9 | 342  | 2 | BE246502 | BE246502 | TCBAP1D47 |
| c1209 | 58.8 | 1.9 | 595  | 5 | BX672477 | BX672477 | BX672477  |
| c1210 | 58.8 | 1.9 | 718  | 7 | CK776486 | CK776486 | 967641 MA |
| 1211  | 58.8 | 1.9 | 814  | 2 | BF348116 | BF348116 | 602022006 |
| 1212  | 58.8 | 1.9 | 944  | 5 | BQ931286 | BQ931286 | AGENCOURT |
| 1213  | 58.6 | 1.9 | 338  | 2 | BE246248 | BE246248 | TCBAP2D06 |
| 1214  | 58.6 | 1.9 | 456  | 4 | BG015017 | BG015017 | PM1-GN018 |
| 1215  | 58.6 | 1.9 | 498  | 1 | AA190645 | AA190645 | zq44a06.r |
| 1216  | 58.6 | 1.9 | 628  | 6 | CB577722 | CB577722 | AMGNNUC:N |
| 1217  | 58.6 | 1.9 | 987  | 2 | BE727277 | BE727277 | 601560955 |
| 1218  | 58.4 | 1.9 | 581  | 5 | BP198298 | BP198298 | BP198298  |
| 1219  | 58.4 | 1.9 | 595  | 1 | AL678465 | AL678465 | AL678465  |
| 1220  | 58.4 | 1.9 | 599  | 1 | AL678560 | AL678560 | AL678560  |
| 1221  | 58.4 | 1.9 | 766  | 4 | BI335382 | BI335382 | 602997946 |
| 1222  | 58.4 | 1.9 | 1109 | 4 | BM547638 | BM547638 | AGENCOURT |
| 1223  | 58.4 | 1.9 | 1121 | 4 | BM477901 | BM477901 | AGENCOURT |
| 1224  | 58.2 | 1.9 | 480  | 5 | BY247585 | BY247585 | BY247585  |
| 1225  | 58.2 | 1.9 | 581  | 5 | BP196129 | BP196129 | BP196129  |
| 1226  | 58.2 | 1.9 | 608  | 1 | AI258757 | AI258757 | LP02029.5 |
| 1227  | 58.2 | 1.9 | 674  | 1 | AU138132 | AU138132 | AU138132  |
| 1228  | 58.2 | 1.9 | 921  | 2 | BF237200 | BF237200 | 602028155 |
| 1229  | 57.8 | 1.8 | 148  | 1 | AV378912 | AV378912 | AV378912  |
| 1230  | 57.8 | 1.8 | 173  | 2 | AW983563 | AW983563 | RC3-HN000 |
| 1231  | 57.8 | 1.8 | 419  | 6 | CB764881 | CB764881 | AMGNNUC:N |
| 1232  | 57.8 | 1.8 | 634  | 6 | CB548205 | CB548205 | AMGNNUC:C |
| 1233  | 57.8 | 1.8 | 634  | 6 | CB577061 | CB577061 | AMGNNUC:C |
| 1234  | 57.8 | 1.8 | 840  | 6 | CB990331 | CB990331 | AGENCOURT |
| 1235  | 57.6 | 1.8 | 253  | 6 | CA394719 | CA394719 | cs55b06.y |
| 1236  | 57.6 | 1.8 | 554  | 4 | BI683327 | BI683327 | 464671 MA |
| 1237  | 57.6 | 1.8 | 574  | 4 | BJ068614 | BJ068614 | BJ068614  |
| 1238  | 57.6 | 1.8 | 631  | 6 | CA876860 | CA876860 | K0951D08- |
| 1239  | 57.6 | 1.8 | 703  | 4 | BJ733929 | BJ733929 | BJ733929  |
| 1240  | 57.6 | 1.8 | 767  | 7 | CO246012 | CO246012 | AGENCOURT |
| 1241  | 57.6 | 1.8 | 911  | 5 | BQ278955 | BQ278955 | AGENCOURT |
| 1242  | 57.4 | 1.8 | 463  | 4 | BI515157 | BI515157 | BB160017B |
| 1243  | 57.4 | 1.8 | 611  | 5 | BX852769 | BX852769 | BX852769  |
| 1244  | 57.4 | 1.8 | 755  | 4 | BG326539 | BG326539 | 602425385 |
| 1245  | 57.4 | 1.8 | 770  | 6 | CA945576 | CA945576 | UI-M-FD0- |
| c1246 | 57.2 | 1.8 | 573  | 2 | BE070335 | BE070335 | QV4-BT040 |
| 1247  | 57.2 | 1.8 | 690  | 1 | AU134748 | AU134748 | AU134748  |
| 1248  | 57.2 | 1.8 | 698  | 5 | BX344176 | BX344176 | BX344176  |
| 1249  | 57.2 | 1.8 | 811  | 7 | CK482600 | CK482600 | AGENCOURT |
| 1250  | 57.2 | 1.8 | 990  | 4 | BI652258 | BI652258 | 603299702 |
| 1251  | 57.2 | 1.8 | 1018 | 4 | BI519944 | BI519944 | 603071726 |
| 1252  | 57   | 1.8 | 444  | 6 | BY531725 | BY531725 | BY531725  |
| 1253  | 57   | 1.8 | 533  | 4 | BI499160 | BI499160 | ie27d02.y |
| 1254  | 57   | 1.8 | 815  | 4 | BI689717 | BI689717 | 603316221 |
| 1255  | 57   | 1.8 | 945  | 7 | CF579434 | CF579434 | AGENCOURT |
| 1256  | 56.8 | 1.8 | 774  | 7 | CN539668 | CN539668 | UI-M-HU0- |
| 1257  | 56.8 | 1.8 | 884  | 2 | BE728944 | BE728944 | 601562382 |
| 1258  | 56.8 | 1.8 | 917  | 4 | BI913405 | BI913405 | 603179004 |
| 1259  | 56.6 | 1.8 | 148  | 2 | BB225254 | BB225254 | BB225254  |
| 1260  | 56.6 | 1.8 | 618  | 7 | CN429152 | CN429152 | 170006000 |
| 1261  | 56.6 | 1.8 | 624  | 6 | CB527987 | CB527987 | UI-M-FY0- |
| c1262 | 56.4 | 1.8 | 148  | 2 | AW045210 | AW045210 | UI-M-BH1- |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 1263  | 56.4 | 1.8 | 561  | 1 | AA929737 | AA929737 | vz05h07.r |
| c1264 | 56.4 | 1.8 | 576  | 2 | BE831264 | BE831264 | PM2-MT004 |
| 1265  | 56.4 | 1.8 | 589  | 7 | CF179045 | CF179045 | 813129 MA |
| 1266  | 56.4 | 1.8 | 907  | 7 | CF583319 | CF583319 | AGENCOURT |
| c1267 | 56.2 | 1.8 | 117  | 2 | BF470020 | BF470020 | UI-M-BH3- |
| 1268  | 56.2 | 1.8 | 222  | 2 | BB548578 | BB548578 | BB548578  |
| 1269  | 56.2 | 1.8 | 794  | 9 | CL640418 | CL640418 | G074D03 G |
| 1270  | 56   | 1.8 | 822  | 5 | BU208115 | BU208115 | 603952728 |
| 1271  | 55.8 | 1.8 | 656  | 6 | CD628627 | CD628627 | 56097394H |
| 1272  | 55.8 | 1.8 | 670  | 1 | AL870127 | AL870127 | AL870127  |
| c1273 | 55.8 | 1.8 | 717  | 7 | CK225357 | CK225357 | 704281487 |
| 1274  | 55.8 | 1.8 | 1051 | 5 | BQ898681 | BQ898681 | AGENCOURT |
| 1275  | 55.6 | 1.8 | 510  | 1 | AA823166 | AA823166 | vw41e06.r |
| 1276  | 55.6 | 1.8 | 596  | 5 | BP872160 | BP872160 | BP872160  |
| 1277  | 55.4 | 1.8 | 307  | 1 | AA354547 | AA354547 | EST62826  |
| 1278  | 55.4 | 1.8 | 391  | 6 | CB775786 | CB775786 | AMGNNUC:N |
| 1279  | 55.4 | 1.8 | 575  | 7 | CN685188 | CN685188 | E0204H04- |
| 1280  | 55.4 | 1.8 | 599  | 5 | BP218578 | BP218578 | BP218578  |
| 1281  | 55.4 | 1.8 | 637  | 1 | AU135310 | AU135310 | AU135310  |
| 1282  | 55.2 | 1.8 | 258  | 1 | AA601686 | AA601686 | no02b07.s |
| c1283 | 55.2 | 1.8 | 428  | 5 | BX683168 | BX683168 | BX683168  |
| 1284  | 55.2 | 1.8 | 647  | 7 | CK338348 | CK338348 | C0629B03- |
| 1285  | 55.2 | 1.8 | 672  | 6 | BY751398 | BY751398 | BY751398  |
| 1286  | 55.2 | 1.8 | 754  | 7 | CN538762 | CN538762 | UI-M-HS0- |
| 1287  | 55.2 | 1.8 | 1066 | 4 | BG542239 | BG542239 | 602571680 |
| 1288  | 55   | 1.7 | 469  | 4 | BG348876 | BG348876 | de74a05.y |
| 1289  | 55   | 1.7 | 546  | 9 | CG594195 | CG594195 | OST252072 |
| 1290  | 54.6 | 1.7 | 683  | 5 | BU269132 | BU269132 | 603506561 |
| 1291  | 54.6 | 1.7 | 938  | 5 | BU150466 | BU150466 | AGENCOURT |
| 1292  | 54.4 | 1.7 | 486  | 2 | BE982860 | BE982860 | UI-M-CG0p |
| 1293  | 54.4 | 1.7 | 711  | 7 | CK694093 | CK694093 | ZF101-P00 |
| 1294  | 54.4 | 1.7 | 745  | 5 | BU345393 | BU345393 | 603523405 |
| c1295 | 54   | 1.7 | 195  | 1 | AI030698 | AI030698 | UI-R-C0-j |
| 1296  | 54   | 1.7 | 573  | 2 | BF550969 | BF550969 | UI-R-C0-j |
| 1297  | 54   | 1.7 | 598  | 6 | CB434784 | CB434784 | 611453 MA |
| 1298  | 54   | 1.7 | 600  | 5 | BU924827 | BU924827 | 7102-54 M |
| 1299  | 54   | 1.7 | 925  | 9 | CNS0091P | AL053013 | Drosophil |
| 1300  | 54   | 1.7 | 1106 | 6 | CD498549 | CD498549 | CDA34-C01 |
| 1301  | 53.8 | 1.7 | 347  | 7 | CN335013 | CN335013 | 170005360 |
| 1302  | 53.8 | 1.7 | 598  | 4 | BI908590 | BI908590 | 603069993 |
| 1303  | 53.8 | 1.7 | 731  | 7 | CR769103 | CR769103 | DKFZp469L |
| 1304  | 53.6 | 1.7 | 651  | 6 | BY722642 | BY722642 | BY722642  |
| 1305  | 53.4 | 1.7 | 1075 | 5 | BM918793 | BM918793 | AGENCOURT |
| c1306 | 53.4 | 1.7 | 1462 | 3 | CR715185 | CR715185 | Tetraodon |
| 1307  | 53.2 | 1.7 | 562  | 7 | CO322494 | CO322494 | EK188241. |
| 1308  | 53.2 | 1.7 | 595  | 1 | AL876266 | AL876266 | AL876266  |
| 1309  | 53.2 | 1.7 | 785  | 7 | CO428820 | CO428820 | UI-M-HX0- |
| 1310  | 53.2 | 1.7 | 987  | 9 | CNS00418 | AL066537 | Drosophil |
| 1311  | 52.8 | 1.7 | 345  | 4 | BG148558 | BG148558 | uu80g02.y |
| 1312  | 52.8 | 1.7 | 488  | 2 | BF773594 | BF773594 | 283122 MA |
| c1313 | 52.8 | 1.7 | 519  | 6 | CB435264 | CB435264 | 615337 MA |
| 1314  | 52.8 | 1.7 | 787  | 4 | BG783400 | BG783400 | SEAUMC003 |
| 1315  | 52.8 | 1.7 | 809  | 5 | BU232264 | BU232264 | 603410226 |
| 1316  | 52.6 | 1.7 | 442  | 7 | CK392174 | CK392174 | K0842D11- |
| c1317 | 52.6 | 1.7 | 493  | 4 | BG009731 | BG009731 | QV1-GN031 |
| 1318  | 52.6 | 1.7 | 564  | 2 | AW659026 | AW659026 | 95939 MAR |
| 1319  | 52.6 | 1.7 | 626  | 1 | AU137591 | AU137591 | AU137591  |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| c1320 | 52.6 | 1.7 | 760  | 5 | BX919359 | BX919359 | BX919359  |
| 1321  | 52.6 | 1.7 | 787  | 5 | BU610933 | BU610933 | UI-M-FC0- |
| 1322  | 52.6 | 1.7 | 817  | 4 | BG342624 | BG342624 | 602374614 |
| 1323  | 52.6 | 1.7 | 870  | 5 | BU612231 | BU612231 | UI-M-EW0- |
| 1324  | 52.6 | 1.7 | 2307 | 9 | AY407762 | AY407762 | Mus muscu |
| 1325  | 52.4 | 1.7 | 428  | 4 | BI882131 | BI882131 | fm85b03.x |
| 1326  | 52.4 | 1.7 | 525  | 2 | BE260428 | BE260428 | 601150894 |
| 1327  | 52.4 | 1.7 | 621  | 4 | BI066930 | BI066930 | pgfln.pk0 |
| 1328  | 52.4 | 1.7 | 688  | 2 | BE385519 | BE385519 | 601278033 |
| 1329  | 52.4 | 1.7 | 699  | 6 | CA327319 | CA327319 | UI-M-FY0- |
| 1330  | 52.4 | 1.7 | 704  | 4 | BG829860 | BG829860 | 602764154 |
| 1331  | 52.4 | 1.7 | 927  | 5 | BU148244 | BU148244 | AGENCOURT |
| 1332  | 52.4 | 1.7 | 938  | 4 | BG830609 | BG830609 | 602767211 |
| 1333  | 52.2 | 1.7 | 387  | 5 | BY093485 | BY093485 | BY093485  |
| 1334  | 52.2 | 1.7 | 740  | 4 | BG831840 | BG831840 | 602765483 |
| 1335  | 52.2 | 1.7 | 938  | 4 | BG422234 | BG422234 | 602446867 |
| 1336  | 52.2 | 1.7 | 962  | 4 | BG324610 | BG324610 | 602422587 |
| 1337  | 52   | 1.7 | 391  | 4 | BJ620346 | BJ620346 | BJ620346  |
| 1338  | 52   | 1.7 | 479  | 4 | BG010829 | BG010829 | IL5-GN024 |
| 1339  | 52   | 1.7 | 814  | 7 | CK476539 | CK476539 | AGENCOURT |
| 1340  | 52   | 1.7 | 2411 | 6 | CB605722 | CB605722 | AMGNNUC:M |
| 1341  | 51.8 | 1.6 | 576  | 4 | BI067451 | BI067451 | pgfln.pk0 |
| 1342  | 51.8 | 1.6 | 687  | 4 | BI916243 | BI916243 | 603178146 |
| 1343  | 51.8 | 1.6 | 751  | 6 | CA317826 | CA317826 | UI-M-FW0- |
| 1344  | 51.6 | 1.6 | 588  | 5 | BP218616 | BP218616 | BP218616  |
| 1345  | 51.6 | 1.6 | 761  | 7 | CO734982 | CO734982 | SLLE04c10 |
| 1346  | 51.6 | 1.6 | 835  | 7 | CO733414 | CO733414 | SLLT02c05 |
| c1347 | 51.4 | 1.6 | 73   | 6 | CD631367 | CD631367 | 56027839H |
| 1348  | 51.4 | 1.6 | 321  | 7 | CO291094 | CO291094 | EK076120. |
| 1349  | 51.4 | 1.6 | 367  | 6 | CD371550 | CD371550 | UI-R-GO0- |
| 1350  | 51.4 | 1.6 | 533  | 5 | BU484169 | BU484169 | 603469842 |
| 1351  | 51.4 | 1.6 | 647  | 4 | BI067436 | BI067436 | pgfln.pk0 |
| 1352  | 51.4 | 1.6 | 743  | 6 | CA326974 | CA326974 | UI-M-FY0- |
| 1353  | 51.4 | 1.6 | 802  | 5 | BU613129 | BU613129 | UI-M-EW0- |
| 1354  | 51.4 | 1.6 | 1929 | 9 | AY403444 | AY403444 | Pan trogl |
| 1355  | 51.2 | 1.6 | 397  | 6 | CB772279 | CB772279 | AMGNNUC:M |
| 1356  | 51.2 | 1.6 | 582  | 5 | BP349308 | BP349308 | BP349308  |
| c1357 | 51.2 | 1.6 | 659  | 1 | AI651838 | AI651838 | wb55h11.x |
| 1358  | 51.2 | 1.6 | 675  | 2 | BF707801 | BF707801 | A379 LE A |
| 1359  | 51.2 | 1.6 | 728  | 1 | AU137554 | AU137554 | AU137554  |
| 1360  | 51.2 | 1.6 | 748  | 1 | AU136052 | AU136052 | AU136052  |
| 1361  | 51.2 | 1.6 | 773  | 5 | BU515916 | BU515916 | AGENCOURT |
| 1362  | 51.2 | 1.6 | 925  | 4 | BG324814 | BG324814 | 602423928 |
| 1363  | 51.2 | 1.6 | 948  | 4 | BG325041 | BG325041 | 602423476 |
| 1364  | 51   | 1.6 | 478  | 7 | CN290121 | CN290121 | 170005319 |
| 1365  | 51   | 1.6 | 563  | 4 | BI791273 | BI791273 | id03h12.y |
| 1366  | 51   | 1.6 | 755  | 1 | AU137539 | AU137539 | AU137539  |
| 1367  | 51   | 1.6 | 774  | 7 | CN537492 | CN537492 | UI-M-HS0- |
| 1368  | 51   | 1.6 | 804  | 7 | CO430718 | CO430718 | UI-M-HX0- |
| 1369  | 51   | 1.6 | 2227 | 9 | AY403443 | AY403443 | Homo sapi |
| 1370  | 51   | 1.6 | 2596 | 3 | AK053115 | AK053115 | Mus muscu |
| 1371  | 50.8 | 1.6 | 650  | 7 | CR429569 | CR429569 | CR429569  |
| 1372  | 50.8 | 1.6 | 671  | 6 | CD295461 | CD295461 | StrPu691. |
| 1373  | 50.8 | 1.6 | 760  | 2 | BF181876 | BF181876 | 601805303 |
| 1374  | 50.4 | 1.6 | 604  | 4 | BI183160 | BI183160 | UNL-P-FN- |
| 1375  | 50.2 | 1.6 | 283  | 7 | CF136469 | CF136469 | UI-HF-BN0 |
| 1376  | 50.2 | 1.6 | 475  | 9 | CL212177 | CL212177 | G033C05 G |

|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 1377  | 50.2 | 1.6 | 836  | 7 | CK600018 | CK600018 | AGENCOURT |
| 1378  | 50   | 1.6 | 505  | 2 | BE487489 | BE487489 | 176253 BA |
| 1379  | 50   | 1.6 | 701  | 6 | CB245456 | CB245456 | UI-M-FY0- |
| 1380  | 50   | 1.6 | 735  | 1 | AU140116 | AU140116 | AU140116  |
| 1381  | 49.8 | 1.6 | 519  | 4 | BM741971 | BM741971 | K-EST0014 |
| 1382  | 49.8 | 1.6 | 805  | 5 | BX844812 | BX844812 | BX844812  |
| 1383  | 49.6 | 1.6 | 300  | 7 | CN255485 | CN255485 | 170004251 |
| 1384  | 49.6 | 1.6 | 410  | 6 | CB803735 | CB803735 | AMGNNUC:N |
| 1385  | 49.6 | 1.6 | 549  | 6 | CB614718 | CB614718 | AMGNNUC:N |
| 1386  | 49.6 | 1.6 | 580  | 5 | BU432018 | BU432018 | 603836176 |
| 1387  | 49.6 | 1.6 | 612  | 7 | CN951333 | CN951333 | Ha_mx0_46 |
| 1388  | 49.6 | 1.6 | 773  | 4 | BI218305 | BI218305 | 602934473 |
| 1389  | 49.4 | 1.6 | 410  | 6 | CB153520 | CB153520 | K-EST0210 |
| c1390 | 49.4 | 1.6 | 423  | 4 | BI058070 | BI058070 | PM4-GN050 |
| 1391  | 49.4 | 1.6 | 516  | 6 | CD619063 | CD619063 | 56053362H |
| 1392  | 49.4 | 1.6 | 516  | 6 | CD619065 | CD619065 | 56053454H |
| c1393 | 49.4 | 1.6 | 538  | 6 | CD619064 | CD619064 | 56053362J |
| c1394 | 49.4 | 1.6 | 550  | 6 | CD619062 | CD619062 | 56053346J |
| c1395 | 49.4 | 1.6 | 551  | 6 | CD619060 | CD619060 | 56053340J |
| c1396 | 49.4 | 1.6 | 552  | 6 | CD619066 | CD619066 | 56053454J |
| 1397  | 49.4 | 1.6 | 559  | 6 | CA872840 | CA872840 | K0920H08- |
| 1398  | 49.4 | 1.6 | 595  | 5 | BP271999 | BP271999 | BP271999  |
| 1399  | 49.4 | 1.6 | 688  | 4 | BI552143 | BI552143 | 603195086 |
| 1400  | 49.4 | 1.6 | 749  | 9 | CNS02V9F | AL215484 | Tetraodon |
| 1401  | 49.4 | 1.6 | 766  | 4 | BG825242 | BG825242 | 602747664 |
| 1402  | 49.4 | 1.6 | 771  | 4 | BI859915 | BI859915 | 603386049 |
| 1403  | 49.4 | 1.6 | 910  | 9 | CNS033DR | AL226008 | Tetraodon |
| 1404  | 49.2 | 1.6 | 542  | 4 | BM740534 | BM740534 | K-EST0011 |
| 1405  | 49.2 | 1.6 | 544  | 4 | BM766233 | BM766233 | K-EST0048 |
| 1406  | 49.2 | 1.6 | 626  | 4 | BM740685 | BM740685 | K-EST0012 |
| c1407 | 49.2 | 1.6 | 897  | 9 | CG766342 | CG766342 | TcB48.4_B |
| c1408 | 49.2 | 1.6 | 898  | 9 | CG770102 | CG770102 | TcB51.2_A |
| c1409 | 49.2 | 1.6 | 901  | 5 | BQ433090 | BQ433090 | AGENCOURT |
| 1410  | 49.2 | 1.6 | 904  | 5 | BQ735037 | BQ735037 | AGENCOURT |
| 1411  | 49.2 | 1.6 | 1177 | 5 | BM906470 | BM906470 | AGENCOURT |
| 1412  | 49.2 | 1.6 | 1309 | 5 | BU541920 | BU541920 | AGENCOURT |
| c1413 | 49   | 1.6 | 293  | 6 | CD631363 | CD631363 | 56027739H |
| c1414 | 49   | 1.6 | 695  | 7 | CK225361 | CK225361 | 704197850 |
| 1415  | 49   | 1.6 | 1161 | 3 | CR679362 | CR679362 | Tetraodon |
| c1416 | 48.8 | 1.6 | 372  | 1 | AA984436 | AA984436 | am86d04.s |
| 1417  | 48.8 | 1.6 | 412  | 6 | CB801382 | CB801382 | AMGNNUC:M |
| 1418  | 48.8 | 1.6 | 473  | 8 | AQ603447 | AQ603447 | HS_2126_A |
| 1419  | 48.8 | 1.6 | 610  | 2 | BB613257 | BB613257 | BB613257  |
| 1420  | 48.8 | 1.6 | 726  | 7 | CN042616 | CN042616 | v11_p43_g |
| 1421  | 48.6 | 1.5 | 431  | 6 | CB757701 | CB757701 | AMGNNUC:M |
| 1422  | 48.6 | 1.5 | 702  | 4 | BI771035 | BI771035 | 603055382 |
| 1423  | 48.6 | 1.5 | 1809 | 3 | AK051165 | AK051165 | Mus muscu |
| 1424  | 48.6 | 1.5 | 3317 | 3 | AK052671 | AK052671 | Mus muscu |
| 1425  | 48.6 | 1.5 | 3672 | 3 | AK028900 | AK028900 | Mus muscu |
| 1426  | 48.6 | 1.5 | 4248 | 3 | AK031704 | AK031704 | Mus muscu |
| 1427  | 48.4 | 1.5 | 416  | 5 | BY224521 | BY224521 | BY224521  |
| 1428  | 48.4 | 1.5 | 539  | 1 | AL918018 | AL918018 | AL918018  |
| 1429  | 48.2 | 1.5 | 428  | 6 | CB794320 | CB794320 | AMGNNUC:N |
| 1430  | 48.2 | 1.5 | 640  | 6 | CA334086 | CA334086 | NISC_ls05 |
| 1431  | 48.2 | 1.5 | 876  | 6 | CA489866 | CA489866 | AGENCOURT |
| 1432  | 48   | 1.5 | 384  | 6 | CB703233 | CB703233 | AMGNNUC:N |
| 1433  | 48   | 1.5 | 569  | 4 | BI775284 | BI775284 | 467707 MA |



|       |      |     |      |   |          |          |           |
|-------|------|-----|------|---|----------|----------|-----------|
| 1434  | 48   | 1.5 | 817  | 7 | CF994909 | CF994909 | AGENCOURT |
| c1435 | 48   | 1.5 | 963  | 5 | BX341410 | BX341410 | BX341410  |
| 1436  | 47.8 | 1.5 | 253  | 4 | BF988853 | BF988853 | IL5-GN017 |
| 1437  | 47.8 | 1.5 | 254  | 4 | BM030705 | BM030705 | 495185 MA |
| 1438  | 47.8 | 1.5 | 406  | 6 | CB808351 | CB808351 | AMGNNUC:S |
| c1439 | 47.8 | 1.5 | 420  | 2 | AW803853 | AW803853 | IL2-UM008 |
| c1440 | 47.8 | 1.5 | 537  | 6 | CB717637 | CB717637 | AMGNNUC:U |
| 1441  | 47.8 | 1.5 | 633  | 7 | CN295126 | CN295126 | 170005326 |
| 1442  | 47.8 | 1.5 | 975  | 2 | BF101157 | BF101157 | 601754732 |
| 1443  | 47.6 | 1.5 | 619  | 4 | BI648895 | BI648895 | 603275856 |
| 1444  | 47.6 | 1.5 | 709  | 6 | CD348531 | CD348531 | UI-M-FY0- |
| 1445  | 47.6 | 1.5 | 777  | 5 | BU708565 | BU708565 | UI-M-FI0- |
| c1446 | 47.6 | 1.5 | 796  | 1 | AL561140 | AL561140 | AL561140  |
| 1447  | 47.6 | 1.5 | 1911 | 9 | AY403382 | AY403382 | Mus muscu |
| c1448 | 47.4 | 1.5 | 240  | 4 | BI000873 | BI000873 | MR3-HN006 |
| c1449 | 47.4 | 1.5 | 469  | 1 | AA859662 | AA859662 | UI-R-E0-b |
| 1450  | 47.4 | 1.5 | 613  | 5 | BX271575 | BX271575 | BX271575  |
| 1451  | 47.2 | 1.5 | 645  | 4 | BI066459 | BI066459 | pgfln.pk0 |
| 1452  | 47.2 | 1.5 | 654  | 2 | BB037994 | BB037994 | BB037994  |
| c1453 | 47.2 | 1.5 | 737  | 9 | CR018931 | CR018931 | Reverse s |
| 1454  | 47.2 | 1.5 | 775  | 5 | BU703431 | BU703431 | UI-M-FO0- |
| 1455  | 47.2 | 1.5 | 1023 | 6 | CD245257 | CD245257 | AGENCOURT |
| c1456 | 47   | 1.5 | 367  | 5 | BQ320183 | BQ320183 | PM4-CT082 |
| 1457  | 47   | 1.5 | 480  | 7 | CR579310 | CR579310 | CR579310  |
| 1458  | 47   | 1.5 | 511  | 4 | BI673056 | BI673056 | ft33e03.y |
| 1459  | 47   | 1.5 | 516  | 6 | CD619061 | CD619061 | 56053346H |
| 1460  | 47   | 1.5 | 543  | 1 | AA940432 | AA940432 | vz48h07.r |
| 1461  | 47   | 1.5 | 625  | 4 | BI753404 | BI753404 | 603026593 |
| 1462  | 47   | 1.5 | 834  | 7 | CF149484 | CF149484 | AGENCOURT |
| 1463  | 46.8 | 1.5 | 350  | 5 | BY200122 | BY200122 | BY200122  |
| 1464  | 46.8 | 1.5 | 365  | 2 | AW437778 | AW437778 | 79230 MAR |
| 1465  | 46.8 | 1.5 | 635  | 1 | AL852575 | AL852575 | AL852575  |
| c1466 | 46.8 | 1.5 | 741  | 2 | BF232471 | BF232471 | de06c04.x |
| 1467  | 46.8 | 1.5 | 932  | 9 | CNS022IX | AL178242 | Tetraodon |
| 1468  | 46.8 | 1.5 | 950  | 5 | BU175283 | BU175283 | AGENCOURT |
| c1469 | 46.8 | 1.5 | 1131 | 5 | BM922197 | BM922197 | AGENCOURT |
| 1470  | 46.6 | 1.5 | 533  | 1 | AA175711 | AA175711 | ms97a05.r |
| 1471  | 46.6 | 1.5 | 609  | 4 | BI066327 | BI066327 | pgfln.pk0 |
| 1472  | 46.6 | 1.5 | 641  | 6 | BY728676 | BY728676 | BY728676  |
| 1473  | 46.6 | 1.5 | 688  | 4 | BG700674 | BG700674 | 602682306 |
| 1474  | 46.4 | 1.5 | 395  | 6 | CB773879 | CB773879 | AMGNNUC:N |
| c1475 | 46.4 | 1.5 | 678  | 9 | CC569313 | CC569313 | CH240_444 |
| 1476  | 46.4 | 1.5 | 957  | 4 | BG261855 | BG261855 | 602373655 |
| 1477  | 46.4 | 1.5 | 971  | 4 | BG342228 | BG342228 | 602374305 |
| c1478 | 46.4 | 1.5 | 985  | 5 | BX402983 | BX402983 | BX402983  |
| 1479  | 46.4 | 1.5 | 994  | 5 | BQ929877 | BQ929877 | AGENCOURT |
| 1480  | 46.2 | 1.5 | 564  | 7 | CK635703 | CK635703 | UI-M-HN0- |
| 1481  | 46.2 | 1.5 | 570  | 2 | BE033028 | BE033028 | 133242 MA |
| 1482  | 46.2 | 1.5 | 590  | 9 | AY420627 | AY420627 | Homo sapi |
| 1483  | 46.2 | 1.5 | 594  | 7 | CN409468 | CN409468 | 170004276 |
| 1484  | 46.2 | 1.5 | 624  | 2 | AW328571 | AW328571 | ds03d12.x |
| 1485  | 46.2 | 1.5 | 634  | 5 | BM951500 | BM951500 | UI-M-EG0- |
| 1486  | 46.2 | 1.5 | 650  | 7 | CF746951 | CF746951 | UI-M-HE0- |
| 1487  | 46.2 | 1.5 | 658  | 7 | CN409465 | CN409465 | 170005325 |
| 1488  | 46.2 | 1.5 | 678  | 7 | CN409457 | CN409457 | 170004177 |
| 1489  | 46.2 | 1.5 | 732  | 7 | CN409463 | CN409463 | 170005325 |
| 1490  | 46.2 | 1.5 | 732  | 7 | CN531114 | CN531114 | UI-M-HO0- |

|       |      |     |      |   |          |                    |
|-------|------|-----|------|---|----------|--------------------|
| 1491  | 46.2 | 1.5 | 741  | 7 | CF730435 | CF730435 UI-M-GZ0- |
| 1492  | 46.2 | 1.5 | 778  | 7 | CF736303 | CF736303 UI-M-HD0- |
| 1493  | 46   | 1.5 | 394  | 6 | CB776561 | CB776561 AMGNNUC:S |
| c1494 | 46   | 1.5 | 428  | 1 | AI458053 | AI458053 tj66h10.x |
| 1495  | 46   | 1.5 | 528  | 2 | BE334076 | BE334076 us29e10.y |
| 1496  | 46   | 1.5 | 575  | 5 | BP338720 | BP338720 BP338720  |
| 1497  | 46   | 1.5 | 714  | 7 | CR789306 | CR789306 DKFZp4590 |
| 1498  | 46   | 1.5 | 2775 | 3 | AK077021 | AK077021 Mus muscu |
| 1499  | 45.8 | 1.5 | 372  | 2 | BF443919 | BF443919 261588 MA |
| 1500  | 45.8 | 1.5 | 375  | 6 | CB691762 | CB691762 AMGNNUC:M |

# ALIGNMENTS

## RESULT 1

CR623694

LOCUS CR623694 3005 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DL005YC17 of B cells (Ramos cell line)  
Cot 25-normalized of Homo sapiens (human).

ACCESSION CR623694

VERSION CR623694.1 GI:50504501

KEYWORDS HTC; CNSLT\_cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3005)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600  
Faraday Avenue

REFERENCE 2 (bases 1 to 3005)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES Location/Qualifiers

source

1. .3005

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DL005YC17"

/tissue\_type="B cells (Ramos cell line) Cot 25-normalized"

/plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 95.6%; Score 3005; DB 3; Length 3005;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 3005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 99  | CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC | 158 |
|    |     |  |     |
| Db | 1   | CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC | 60  |
| Qy | 159 | TTCCAAGTCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCC    | 218 |
|    |     |  |     |
| Db | 61  | TTCCAAGTCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCC    | 120 |
| Qy | 219 | ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG | 278 |
|    |     |  |     |
| Db | 121 | ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG | 180 |
| Qy | 279 | AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG | 338 |
|    |     |  |     |
| Db | 181 | AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG | 240 |
| Qy | 339 | GGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGGATCCAGGGGTCCCAGGCTAAAG   | 398 |
|    |     |  |     |
| Db | 241 | GGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGGATCCAGGGGTCCCAGGCTAAAG   | 300 |
| Qy | 399 | AACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAG  | 458 |
|    |     |  |     |
| Db | 301 | AACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAG  | 360 |
| Qy | 459 | AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCAT   | 518 |
|    |     |  |     |
| Db | 361 | AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCAT   | 420 |
| Qy | 519 | CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGAT | 578 |
|    |     |  |     |
| Db | 421 | CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGAT | 480 |
| Qy | 579 | TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCTTT  | 638 |
|    |     |  |     |
| Db | 481 | TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCTTT  | 540 |
| Qy | 639 | GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG | 698 |
|    |     |  |     |
| Db | 541 | GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG | 600 |
| Qy | 699 | AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC | 758 |
|    |     |  |     |
| Db | 601 | AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC | 660 |
| Qy | 759 | AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT | 818 |
|    |     |  |     |
| Db | 661 | AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT | 720 |
| Qy | 819 | TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG | 878 |
|    |     |  |     |
| Db | 721 | TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG | 780 |
| Qy | 879 | AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG | 938 |
|    |     |  |     |
| Db | 781 | AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG | 840 |

|    |      |   |      |
|----|------|---|------|
| Qy | 939  | CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAG   | 998  |
|    |      |   |      |
| Db | 841  | CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAG   | 900  |
| Qy | 999  | CTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCC    | 1058 |
|    |      |   |      |
| Db | 901  | CTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCC    | 960  |
| Qy | 1059 | CACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTT  | 1118 |
|    |      |   |      |
| Db | 961  | CACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTT  | 1020 |
| Qy | 1119 | TGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAAC  | 1178 |
|    |      |   |      |
| Db | 1021 | TGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAAC  | 1080 |
| Qy | 1179 | AAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGT   | 1238 |
|    |      |   |      |
| Db | 1081 | AAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGT   | 1140 |
| Qy | 1239 | TGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATG | 1298 |
|    |      |   |      |
| Db | 1141 | TGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATG | 1200 |
| Qy | 1299 | GATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT   | 1358 |
|    |      |   |      |
| Db | 1201 | GATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT   | 1260 |
| Qy | 1359 | GCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACC   | 1418 |
|    |      |   |      |
| Db | 1261 | GCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACC   | 1320 |
| Qy | 1419 | ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA  | 1478 |
|    |      |   |      |
| Db | 1321 | ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA  | 1380 |
| Qy | 1479 | GAGATTAGCTGTTCCCTGACCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAG      | 1538 |
|    |      |   |      |
| Db | 1381 | GAGATTAGCTGTTCCCTGACCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAG      | 1440 |
| Qy | 1539 | GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAAGTGTAGT  | 1598 |
|    |      |   |      |
| Db | 1441 | GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAAGTGTAGT  | 1500 |
| Qy | 1599 | GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCT | 1658 |
|    |      |   |      |
| Db | 1501 | GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCT | 1560 |
| Qy | 1659 | GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATG   | 1718 |
|    |      |   |      |
| Db | 1561 | GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATG   | 1620 |
| Qy | 1719 | GAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT   | 1778 |
|    |      |   |      |
| Db | 1621 | GAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT   | 1680 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1779 | CAGAGCCGCCCCGAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC    | 1838 |
|    |      |  |      |
| Db | 1681 | CAGAGCCGCCCCGAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC    | 1740 |
| Qy | 1839 | CCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC    | 1898 |
|    |      |  |      |
| Db | 1741 | CCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC    | 1800 |
| Qy | 1899 | CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT   | 1958 |
|    |      |  |      |
| Db | 1801 | CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT   | 1860 |
| Qy | 1959 | GGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC   | 2018 |
|    |      |  |      |
| Db | 1861 | GGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC   | 1920 |
| Qy | 2019 | TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGG   | 2078 |
|    |      |  |      |
| Db | 1921 | TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGG   | 1980 |
| Qy | 2079 | GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG   | 2138 |
|    |      |  |      |
| Db | 1981 | GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG   | 2040 |
| Qy | 2139 | TCCTACTGGCCCCACTTTTGTCACTGTCACTGTCCCTCTTTGCCTTAGTGCTTTCAGGAGCC | 2198 |
|    |      |  |      |
| Db | 2041 | TCCTACTGGCCCCACTTTTGTCACTGTCACTGTCCCTCTTTGCCTTAGTGCTTTCAGGAGCC | 2100 |
| Qy | 2199 | CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGC   | 2258 |
|    |      |  |      |
| Db | 2101 | CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGC   | 2160 |
| Qy | 2259 | TGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCT    | 2318 |
|    |      |  |      |
| Db | 2161 | TGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCT    | 2220 |
| Qy | 2319 | CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACT   | 2378 |
|    |      |  |      |
| Db | 2221 | CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACT   | 2280 |
| Qy | 2379 | GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG   | 2438 |
|    |      |  |      |
| Db | 2281 | GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG   | 2340 |
| Qy | 2439 | CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC   | 2498 |
|    |      |  |      |
| Db | 2341 | CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC   | 2400 |
| Qy | 2499 | CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG   | 2558 |
|    |      |  |      |
| Db | 2401 | CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG   | 2460 |
| Qy | 2559 | CAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGG   | 2618 |
|    |      |  |      |
| Db | 2461 | CAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGG   | 2520 |
| Qy | 2619 | GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT   | 2678 |

|    |      |  |      |
|----|------|--|------|
|    |      |  |      |
| Db | 2521 | GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT   | 2580 |
| Qy | 2679 | TCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTCAGAGACCCTAAAAAACCTGC     | 2738 |
|    |      |  |      |
| Db | 2581 | TCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTCAGAGACCCTAAAAAACCTGC     | 2640 |
| Qy | 2739 | CTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGC   | 2798 |
|    |      |  |      |
| Db | 2641 | CTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGC   | 2700 |
| Qy | 2799 | CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAG   | 2858 |
|    |      |  |      |
| Db | 2701 | CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAG   | 2760 |
| Qy | 2859 | GGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCA   | 2918 |
|    |      |  |      |
| Db | 2761 | GGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCA   | 2820 |
| Qy | 2919 | GGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGGCAGACTCTGAT    | 2978 |
|    |      |  |      |
| Db | 2821 | GGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGGCAGACTCTGAT    | 2880 |
| Qy | 2979 | CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG   | 3038 |
|    |      |  |      |
| Db | 2881 | CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG   | 2940 |
| Qy | 3039 | CTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTTCAGAAAACCTGCTTG | 3098 |
|    |      |  |      |
| Db | 2941 | CTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTTCAGAAAACCTGCTTG | 3000 |
| Qy | 3099 | TCAGA  | 3103 |
|    |      |  |      |
| Db | 3001 | TCAGA  | 3005 |

## RESULT 2

HSM807023

LOCUS HSM807023 3151 bp mRNA linear HTC 22-SEP-2004

DEFINITION Homo sapiens mRNA; cDNA DKFZp686D04248 (from clone DKFZp686D04248).

ACCESSION BX640891

VERSION BX640891.1 GI:34365195

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3151)

AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

CONSRM The German cDNA Consortium

TITLE Direct Submission

JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;



|    |      |  |      |
|----|------|--|------|
| Qy | 322  | GAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAG | 381  |
|    |      |  |      |
| Db | 320  | GAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAG | 379  |
| Qy | 382  | GGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAAT | 441  |
|    |      |  |      |
| Db | 380  | GGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAAT | 439  |
| Qy | 442  | GTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTT | 501  |
|    |      |  |      |
| Db | 440  | GTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTT | 499  |
| Qy | 502  | CTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCT | 561  |
|    |      |  |      |
| Db | 500  | CTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCT | 559  |
| Qy | 562  | TCATTGAACTTCAAGATTCTTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAA | 621  |
|    |      |  |      |
| Db | 560  | TCATTGAACTTCAAGATTCTTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAA | 619  |
| Qy | 622  | AAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGC | 681  |
|    |      |  |      |
| Db | 620  | AAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGC | 679  |
| Qy | 682  | TCTATTCTGGTACTATGAACAACCTTCTGGGCAGTGAGCCCATCCTGATGCGCACACTGG | 741  |
|    |      |  |      |
| Db | 680  | TCTATTCTGGTACTATGAACAACCTTCTGGGCAGTGAGCCCATCCTGATGCGCACACTGG | 739  |
| Qy | 742  | GATCCCAGCCTGTCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCTCCT  | 801  |
|    |      |  |      |
| Db | 740  | GATCCCAGCCTGTCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCTCCT  | 799  |
| Qy | 802  | TTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCG | 861  |
|    |      |  |      |
| Db | 800  | TTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCG | 859  |
| Qy | 862  | AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG | 921  |
|    |      |  |      |
| Db | 860  | AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG | 919  |
| Qy | 922  | TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCT  | 981  |
|    |      |  |      |
| Db | 920  | TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCT  | 979  |
| Qy | 982  | GCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCG   | 1041 |
|    |      |  |      |
| Db | 980  | GCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCG   | 1039 |
| Qy | 1042 | ATTCTCCCACAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGA  | 1101 |
|    |      |  |      |
| Db | 1040 | ATTCTCCCACAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGA  | 1099 |
| Qy | 1102 | CCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGA | 1161 |
|    |      |  |      |
| Db | 1100 | CCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGA | 1159 |
| Qy | 1162 | AATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCA  | 1221 |



|    |      |   |      |
|----|------|---|------|
| Db | 1160 | <br>AATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCA   | 1219 |
| Qy | 1222 | ACCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGA      | 1281 |
| Db | 1220 | <br>ACCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGA  | 1279 |
| Qy | 1282 | AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCG     | 1341 |
| Db | 1280 | <br>AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCG | 1339 |
| Qy | 1342 | TGGAGTATACACGGCTTGCACTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTG      | 1401 |
| Db | 1340 | <br>TGGAGTATACACGGCTTGCACTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTG  | 1399 |
| Qy | 1402 | TCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCA      | 1461 |
| Db | 1400 | <br>TCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCA  | 1459 |
| Qy | 1462 | GTGCTCATCTGGTGGAAGAGATTAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGC      | 1521 |
| Db | 1460 | <br>GTGCTCATCTGGTGGAAGAGATTAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGC  | 1519 |
| Qy | 1522 | AGCTGGCCCCCACCAGGGTGCACTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGC       | 1581 |
| Db | 1520 | <br>AGCTGGCCCCCACCAGGGTGCACTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGC   | 1579 |
| Qy | 1582 | CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGTGCCCCGAGCCCC      | 1641 |
| Db | 1580 | <br>CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGTGCCCCGAGCCCC  | 1639 |
| Qy | 1642 | ACTGTGCCTGGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACT        | 1701 |
| Db | 1640 | <br>ACTGTGCCTGGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACT    | 1699 |
| Qy | 1702 | CCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGA      | 1761 |
| Db | 1700 | <br>CCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGA  | 1759 |
| Qy | 1762 | GCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCTGGCTGTCCCCA        | 1821 |
| Db | 1760 | <br>GCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCTGGCTGTCCCTA    | 1819 |
| Qy | 1822 | ACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTC       | 1881 |
| Db | 1820 | <br>ACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTC   | 1879 |
| Qy | 1882 | ATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGA      | 1941 |
| Db | 1880 | <br>ATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGA  | 1939 |
| Qy | 1942 | TAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCAT      | 2001 |
| Db | 1940 | <br>TAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCAT  | 1999 |
| Qy | 2002 | ACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAC      | 2061 |
|    |      |   |      |

|    |      |   |      |
|----|------|---|------|
| Db | 2000 | ACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAAC    | 2059 |
| Qy | 2062 | TGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG     | 2121 |
|    |      |   |      |
| Db | 2060 | TGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG     | 2119 |
| Qy | 2122 | CCCTGGCTGCCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCT    | 2181 |
|    |      |   |      |
| Db | 2120 | CCCTGGCTGCCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCT    | 2179 |
| Qy | 2182 | TAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCCTCCCCATTGAGAGCACTCCGGGCTC  | 2241 |
|    |      |   |      |
| Db | 2180 | TAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCCTCCCCATTGAGAGCACTCCGGGCTC  | 2239 |
| Qy | 2242 | GGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAG   | 2301 |
|    |      |   |      |
| Db | 2240 | GGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAG   | 2299 |
| Qy | 2302 | AGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACA    | 2361 |
|    |      |   |      |
| Db | 2300 | AGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACA    | 2359 |
| Qy | 2362 | ACAACCTGCCCTAGGCACCTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAG | 2421 |
|    |      |   |      |
| Db | 2360 | ACAACCTGCCCTAGGCACCTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAG | 2419 |
| Qy | 2422 | GCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCAC    | 2481 |
|    |      |   |      |
| Db | 2420 | GCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCAC    | 2479 |
| Qy | 2482 | AAAAGACCACCTTTCTCCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTC   | 2541 |
|    |      |   |      |
| Db | 2480 | AAAAGACCACCTTTCTCCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTC   | 2539 |
| Qy | 2542 | AGCAGGGTGATGCACAGCAGTCTGCCTCCCCCTATGGGACTCCCTTCTACCAAGCACATGA   | 2601 |
|    |      |   |      |
| Db | 2540 | AGCAGGGTGATGCACAGCAGTCTGCCTCCCCCTATGGGACTCCCTTCTACCAAGCACATGA   | 2599 |
| Qy | 2602 | GCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCT    | 2661 |
|    |      |   |      |
| Db | 2600 | GCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCT    | 2659 |
| Qy | 2662 | GGAGAGGATCCTTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTCAAGA  | 2721 |
|    |      |   |      |
| Db | 2660 | GGAGAGGATCCTTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTCAAGA  | 2719 |
| Qy | 2722 | GACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACA    | 2781 |
|    |      |   |      |
| Db | 2720 | GACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACA    | 2779 |
| Qy | 2782 | ATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCA    | 2841 |
|    |      |   |      |
| Db | 2780 | ATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCA    | 2839 |
| Qy | 2842 | ACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCG    | 2901 |
|    |      |   |      |
| Db | 2840 | ACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCG    | 2899 |

Qy 2902 TGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAG 2961  
 |||  
 Db 2900 TGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAG 2959  
 Qy 2962 TTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT 3021  
 |||  
 Db 2960 TTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT 3019  
 Qy 3022 TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCCTTTGTTTTGGG 3081  
 |||  
 Db 3020 TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCCTTTGTTTTGGG 3079  
 Qy 3082 ATTCAGAAAAGTCTGCTTGTCTGAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAA 3141  
 |||  
 Db 3080 ATTCAGAAAAGTCTGCTTGTCTGAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAA 3139  
 Qy 3142 AA 3143  
 ||  
 Db 3140 AA 3141

### RESULT 3

AY402621

LOCUS AY402621 2172 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY402621

VERSION AY402621.1 GI:39758607

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2172)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2172)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .2172  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"

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gene                /db_xref="taxon:9606"
                   <1..>2172
                   /locus_tag="HCM1285"
ORIGIN
Query Match          59.6%;  Score 1874;  DB 9;  Length 2172;
Best Local Similarity 86.3%;  Pred. No. 0;
Matches 1874;  Conservative 0;  Mismatches 298;  Indels 0;  Gaps 0;

Qy      105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1  ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 60

Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 224
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy      345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 300

Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 420

Qy      525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTTAC 584
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTTAC 480

Qy      585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCCTTTGACCCC 644
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCCTTTGACCCC 540

Qy      645 GCTCACAAGCATAACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCTCACAAGCATAACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 600

Qy      705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 764
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 660

Qy      765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
         ||||||||||||||||||||||||||||
Db      661 GACAACTTCCTCCGCTGGCTGCATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

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|    |      |  |      |
|----|------|--|------|
| Qy | 825  | CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGGCTC      | 884  |
| Db | 721  | NNN      | 780  |
| Qy | 885  | CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGC GGCGAAAAGCTGCTGCAG      | 944  |
| Db | 781  | NNN      | 840  |
| Qy | 945  | AAGAAGTGGACCACCTTCCTGAAGGCC CAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC      | 1004 |
| Db | 841  | NNN      | 900  |
| Qy | 1005 | TTCAACGT CATCCGCCACGCGGT CCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC     | 1064 |
| Db | 901  | NNN      | 960  |
| Qy | 1065 | TACGCAGTCTTCACCTCC CAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC<br>  | 1124 |
| Db | 961  | NNNNNNNNNNNNNNNNNNNNNNNGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC       | 1020 |
| Qy | 1125 | TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA<br>   | 1184 |
| Db | 1021 | TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA       | 1080 |
| Qy | 1185 | ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCA<br>    | 1244 |
| Db | 1081 | ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCA        | 1140 |
| Qy | 1245 | GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG<br>  | 1304 |
| Db | 1141 | GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG      | 1200 |
| Qy | 1305 | CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTG CAGTG<br>  | 1364 |
| Db | 1201 | CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTG CAGTG      | 1260 |
| Qy | 1365 | GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA<br>   | 1424 |
| Db | 1261 | GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA       | 1320 |
| Qy | 1425 | GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT<br>   | 1484 |
| Db | 1321 | GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT       | 1380 |
| Qy | 1485 | CAGCTGTTCCCTGACCCTGAACCTG TTCGCAACCTGCAGCTGGCCCCCCACCCAGGGTGCA<br> | 1544 |
| Db | 1381 | CAGCTGTTCCCTGACCCTGAACCTG TTCGCAACCTGCAGCTGGCCCCCCACCCAGGGTGCA     | 1440 |
| Qy | 1545 | GTGTTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCA ACTGTAGTGTCTAT<br> | 1604 |
| Db | 1441 | GTGTTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCA ACTGTAGTGTCTAT     | 1500 |
| Qy | 1605 | GAGAGCTGTGTGGACTGTGTCTTG CCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC<br>   | 1664 |
| Db | 1501 | GAGAGCTGTGTGGACTGTGTCTTG CCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC       | 1560 |
| Qy | 1665 | CGAACCTGTTGCCTCCTGTCTG CCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG      | 1724 |

|    |      |   |      |
|----|------|---|------|
|    |      |   |      |
| Db | 1561 | CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGG   | 1620 |
| Qy | 1725 | GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC  | 1784 |
|    |      |   |      |
| Db | 1621 | GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC  | 1680 |
| Qy | 1785 | CGCCCGCAAATCATTAAGAAGTCCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC  | 1844 |
|    |      |   |      |
| Db | 1681 | CGCCCGCAAATCATTAAGAAGTCCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC  | 1740 |
| Qy | 1845 | CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA  | 1904 |
|    |      |   |      |
| Db | 1741 | CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA  | 1800 |
| Qy | 1905 | GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT  | 1964 |
|    |      |   |      |
| Db | 1801 | GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT  | 1860 |
| Qy | 1965 | CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG  | 2024 |
|    |      |   |      |
| Db | 1861 | CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG  | 1920 |
| Qy | 2025 | GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT   | 2084 |
|    |      |   |      |
| Db | 1921 | GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT   | 1980 |
| Qy | 2085 | GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC  | 2144 |
|    |      |   |      |
| Db | 1981 | GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC  | 2040 |
| Qy | 2145 | TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC   | 2204 |
|    |      |   |      |
| Db | 2041 | TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC   | 2100 |
| Qy | 2205 | ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG | 2264 |
|    |      |   |      |
| Db | 2101 | ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG | 2160 |
| Qy | 2265 | ACCCTGCGCCCT  | 2276 |
|    |      |   |      |
| Db | 2161 | ACCCTGCGCCCT  | 2172 |

# RESULT 4

AY402622

LOCUS AY402622 2133 bp DNA linear GSS 12-DEC-2003

DEFINITION Pan troglodytes HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY402622

VERSION AY402622.1 GI:39758608

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 2133)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2133)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .2133

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

gene <1. .>2133

/locus\_tag="HCM1285"

# ORIGIN

Query Match 56.2%; Score 1765.4; DB 9; Length 2133;

Best Local Similarity 82.9%; Pred. No. 0;

Matches 1769; Conservative 0; Mismatches 364; Indels 0; Gaps 0;

Qy 105 ATGGCCCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCCCTTTTCCTCTTCCAA 164

Db 1 ATGGCCCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCCCTTTTCCTCTTCCAA 60

Qy 165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCCATGCCC 224

Db 61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGANNCGGGCAGGGGCCCCATGCCC 120

Qy 225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284

Db 121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy 285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344

Db 181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy 345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG 404

Db 241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG 300

Qy 405 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464

Db 301 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy 465 GAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524

|    |      |  |      |
|----|------|--|------|
| Db | 361  | GAGACACAGTGTTCCTCAACTTCATCCGCTGCTCCTGGTTTCTTACAATGTCAACCATCTCTAC | 420  |
| Qy | 525  | ACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTAACCTTCATTGAACCTCAAGATTCTCTAC  | 584  |
| Db | 421  |  | 480  |
| Qy | 585  | CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGGAAAAGGCCAAAGCCCCTTTGACCCCC   | 644  |
| Db | 481  |  | 540  |
| Qy | 645  | GCTCACAAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC    | 704  |
| Db | 541  |  | 600  |
| Qy | 705  | TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCTCAAGACC    | 764  |
| Db | 601  |  | 660  |
| Qy | 765  | GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC     | 824  |
| Db | 661  |  | 720  |
| Qy | 825  | CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC     | 884  |
| Db | 721  | NN   | 780  |
| Qy | 885  | CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG     | 944  |
| Db | 781  | NN   | 840  |
| Qy | 945  | AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC      | 1004 |
| Db | 841  | NN   | 900  |
| Qy | 1005 | TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC      | 1064 |
| Db | 901  | NN   | 960  |
| Qy | 1065 | TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC     | 1124 |
| Db | 961  |  | 1020 |
| Qy | 1125 | TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA     | 1184 |
| Db | 1021 |  | 1080 |
| Qy | 1185 | ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA     | 1244 |
| Db | 1081 |  | 1140 |
| Qy | 1245 | GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG    | 1304 |
| Db | 1141 |  | 1200 |
| Qy | 1305 | CAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAAGTG     | 1364 |
| Db | 1201 |  | 1260 |
| Qy | 1261 | CAGGTGGTAGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAAGTG     | 1320 |



|    |      |   |      |
|----|------|---|------|
| Qy | 1365 | GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA  | 1424 |
|    |      |   |      |
| Db | 1261 | GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA  | 1320 |
| Qy | 1425 | GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT  | 1484 |
|    |      |   |      |
| Db | 1321 | GGGTCGNTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAANNNNNTT | 1380 |
| Qy | 1485 | CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCA    | 1544 |
|    |      |   |      |
| Db | 1381 | CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCA    | 1440 |
| Qy | 1545 | GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTAT  | 1604 |
|    |      |   |      |
| Db | 1441 | GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTAT  | 1500 |
| Qy | 1605 | GAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC   | 1664 |
|    |      |   |      |
| Db | 1501 | GAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGATCCTGAGTCC   | 1560 |
| Qy | 1665 | CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG   | 1724 |
|    |      |   |      |
| Db | 1561 | CGAACCTGTTGCCTCCTNNNNNNNNNNNNNNNGAACTCCTGGAAGCAGGACATGGAGCGG  | 1620 |
| Qy | 1725 | GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC  | 1784 |
|    |      |   |      |
| Db | 1621 | GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC  | 1680 |
| Qy | 1785 | CGCCCGCAAATCATTAAGAAGTCCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC  | 1844 |
|    |      |   |      |
| Db | 1681 | CGCCCGCAAATCATTAAGAAGTCCCTGGCTGTCCCTAACTCCATCCTGGAGNTCCCCTGC  | 1740 |
| Qy | 1845 | CCCCACCTGTCAGCCTTGCCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA  | 1904 |
|    |      |   |      |
| Db | 1741 | CCCCACCTGTCAGCCTTGCCCTCTTACTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA  | 1800 |
| Qy | 1905 | GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT  | 1964 |
|    |      |   |      |
| Db | 1801 | GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT  | 1860 |
| Qy | 1965 | CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG  | 2024 |
|    |      |   |      |
| Db | 1861 | CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG  | 1920 |
| Qy | 2025 | GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT   | 2084 |
|    |      |   |      |
| Db | 1921 | GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT   | 1980 |
| Qy | 2085 | GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTAC  | 2144 |
|    |      |   |      |
| Db | 1981 | GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTAC  | 2040 |
| Qy | 2145 | TGGCCCCACTTTGTCACTGTCAGTGTCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATC  | 2204 |
|    |      |   |      |
| Db | 2041 | TGGCCCCACTTTGTCACTGTCAGTGTCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATC  | 2100 |

Qy 2205 ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGG 2237  
 ||||| ||||| ||||| |||||  
 Db 2101 ATCCTCNTGGCCTCCCCANNGAGAGCACTCCGG 2133

## RESULT 5

AK077976

|       |          |         |      |        |                 |
|-------|----------|---------|------|--------|-----------------|
| LOCUS | AK077976 | 3206 bp | mRNA | linear | HTC 03-APR-2004 |
|-------|----------|---------|------|--------|-----------------|

**DEFINITION** Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030492A12 product:sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A, full insert sequence.

ACCESSION AK077976

VERSION AK077976.1 GI:26097602

**KEYWORDS** HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM *Mus musculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

|       |  |
|-------|--|
| TITLE | RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer |
|-------|--|

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

## REFERENCE

**AUTHORS** The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

## REFERENCE

**AUTHORS** The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs

JOURNAL Nature 420, 563–573 (2002)

REFERENCE 6 (bases 1 to 3206)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES

source Location/Qualifiers

1. .3206

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="FANTOM\_DB:6030492A12"

/db\_xref="taxon:10090"

/clone="6030492A12"

/sex="male"

/tissue\_type="testis"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="13 days embryo"

misc\_feature 224. .2507

/note="putative

sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A (MGD|MGI:107560, GB|NM\_013658, evidence: BLASTN, 99%, match=2517)"

polyA\_signal 3181. .3186

/note="putative"

polyA\_site 3206

/note="putative"

ORIGIN

Query Match 55.6%; Score 1747.4; DB 3; Length 3206;

Best Local Similarity 76.7%; Pred. No. 0;

Matches 2355; Conservative 0; Mismatches 621; Indels 95; Gaps 14;

|    |     |   |      |
|----|-----|---|------|
| Qy | 75  | GAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCTGGACCCC   | 134  |
| Db | 194 | GAACCATCTGGTGACCATCTCAGGCTGACCATGGCCCTACCATCCCTGGGCCAGGACTCA  | 253  |
| Qy | 135 | TGGAGCCTCCTGGGCCTTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACC  | 194  |
| Db | 254 | TGGAGTCTCCTGCGTGTTTTTTTCTTCCAACCTTCTCCTGCTGCCATCACTGCCACCTGCT | 313  |
| Qy | 195 | GCGGGGGGAGGCGGGCAGGGGCCCATGCCAGGGTCAGATACTATGCAGGGGATGAACGT   | 254  |
| Db | 314 | TCTGGGACTGGTGGTCAGGGGCCCATGCCAGAGTCAAATACCATGCTGGAGACGGGCAC   | 373  |
| Qy | 255 | AGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTGACACTCTGCTCCTGAGT   | 314  |
| Db | 374 | AGGGCCCTCAGCTTCTTCCAACAAAAGGCCCTCCGAGACTTTGACACGCTGCTCCTGAGT  | 433  |
| Qy | 315 | GGTGATGGAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGAATATCCAG  | 374  |
| Db | 434 | GACGATGGCAACACTCTCTATGTGGGGGCTCGAGAGGCCGTCTTGGCCTTGAATATCCAG  | 493  |
| Qy | 375 | GATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAG  | 434  |
| Db | 494 | AACCCAGGAATCCCAAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGAGAGAAAAAAG  | 553  |
| Qy | 435 | AGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTC  | 494  |
| Db | 554 | ACCGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATTTCGAGTC | 613  |
| Qy | 495 | CTGGTTTCTTACAATGTACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCT   | 554  |
| Db | 614 | CTGGTCTCTTACAATGCTACTCACCTCTATGCCTGTGGGACCTTTCGCCTTCAGCCCTGCC | 673  |
| Qy | 555 | TGTACCTTCATTGAACTTCAAGATTCCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATG | 614  |
| Db | 674 | TGTACCTTCATTGAACTCCAAGATTCCCTCCTGTTGCCCATCTTGATAGACAAGGTCATG  | 733  |
| Qy | 615 | GAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGAT  | 674  |
| Db | 734 | GACGGGAAGGGCCAAAGCCCCTTTGACCTGTTACAAGCACACAGCTGTCTTGGTCGAT    | 793  |
| Qy | 675 | GGGATGCTCTATTCTGGTACTATGAACAACCTTCTGGGCAGTGAGCCCATCCTGATGCGC  | 734  |
| Db | 794 | GGGATGCTTTATTCCGGCACCATGAACAACCTTCTGGGCAGCGAGCCCATCCTGATGCGG  | 853  |
| Qy | 735 | ACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGAC   | 794  |
| Db | 854 | ACACTGGGATCCCAGCCTGTTCTCAAGACTGACATCTTCTTACGCTGGCTGCACGCGGAT  | 913  |
| Qy | 795 | GCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACA  | 854  |
| Db | 914 | GCCTCCTTCGTGGCAGCCATTCCATCCACCCAGGTCGTCTATTCTTCTTTGAGGAGACA   | 973  |
| Qy | 855 | GCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAG  | 914  |
| Db | 974 | GCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGGTGGCTCAAGTCTGCAAG  | 1033 |
| Qy | 915 | AATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCTGAAAGGCCAG   | 974  |

Db 1034 AACGACGTGGGCGGTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTCAAAGCCAG 1093  
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 Db 1094 TTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCCGCCACGCGGTCTTGCTG 1153  
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Db 1931 AGTCCCCAACTCCATCCTGGAGCTGCCCTGCCCCACCTGTCAGCACTGGCCTCTTACCA 1990

Qy 1874 TTGGAGTCATGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT 1933  
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Db 1991 CTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGGCTCCCT 2050

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Db 2051 CTTGCTGCTGCCGAGGATGGTGTGCGAGGCCCTCTACCAGTGTGTGGCGACTGAGAACGG 2110

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# RESULT 6

AK035918

LOCUS AK035918 3086 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630018D15 product:sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A, full insert sequence.

ACCESSION AK035918

VERSION AK035918.1 GI:26084904

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE 6 (bases 1 to 3086)  
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)  
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.



Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site for further details.

URL:<http://genome.gsc.riken.jp/>

URL:<http://fantom.gsc.riken.jp/>.

FEATURES  
source Location/Qualifiers  
1. .3086  
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/db\_xref="taxon:10090"  
/clone="9630018D15"  
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/dev\_stage="16 days neonate"  
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/note="putative  
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/note="putative"  
polyA\_site 3086  
/note="putative"

#### ORIGIN

Query Match 54.1%; Score 1701.4; DB 3; Length 3086;  
Best Local Similarity 75.2%; Pred. No. 0;  
Matches 2364; Conservative 0; Mismatches 637; Indels 141; Gaps 14;

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Qy     230 CAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCA 289
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Qy     290 GGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGA 349
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| Qy | 723  | ATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCTCCGCTGG    | 782  |
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| Db | 964  | CTCAAAGCCCAGTTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCCGCCAC   | 1023 |
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| Qy | 2163 | GTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCA     | 2222 |
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| Db | 2281 | AAGGCTCCACTGAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCC     | 2340 |
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| Db | 2341 | AGTGACGTAGATGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAG     | 2400 |
| Qy | 2403 | GGCCGGGGCT--GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC     | 2460 |
| Db | 2401 | ATCCGCAGCTGAGCAGAGCAAGCCACTGGCCTTGTTGGCTATGC-----                | 2444 |
| Qy | 2461 | TGACTAGGATGACAGCAGCACAAAAGACCACCTTCTCCCTGAGAGGAGCTTCTGCTAC       | 2520 |
| Db | 2445 | -----CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAA               | 2489 |
| Qy | 2521 | TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC     | 2580 |
| Db | 2490 | CGTGTGTACCTACAGCACCCAGTAGGT-----CCTCCCCTGTGGGAC                  | 2532 |
| Qy | 2581 | TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC     | 2640 |
| Db | 2533 | TCTCTTCTGCAAGCACATTGGGCTGTCT-----CCATACCTGTACT                   | 2573 |
| Qy | 2641 | TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC     | 2700 |
| Db | 2574 | TGTGCTGTGACAGGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTC     | 2633 |
| Qy | 2701 | CAGAAACACAGTGTTTCAAGAGACCCTAAAAACCTGCCTGTCCCAGGACCCTATGGTAA      | 2760 |
| Db | 2634 | CTGTAACAAACGTGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGA     | 2693 |
| Qy | 2761 | TGAACACCAAACATCTAAACAATCATATGCTA-----ACATGCCACTCCTGGAAACTC       | 2813 |
| Db | 2694 | CAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCCCTGCAAACCTCCATCCTGAACGCTGT   | 2752 |
| Qy | 2814 | CACTCT----GAAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAG     | 2868 |
| Db | 2753 | CACTCTAGAAGCAGCTGCTGCTTTGAACACCAGCCCACCTCCTTCCCAAGAGTCTCTAT      | 2812 |
| Qy | 2869 | GGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTT     | 2928 |
| Db | 2813 | GGAGTTGGCCCCCTTGTTTTCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATC     | 2869 |

|      |      |   |      |
|------|------|---|------|
| Qy   | 2929 | CCTGAAGTCTGACCACCTTTTCCTTGCTTCAGTTGGGGCAGACTCTGATCCCT--- <td style="text-align: left; vertical-align: top;">2985</td> | 2985 |
|      |      |   |      |
| Db   | 2870 | TCTGAAGTCTAACCACCTTCCTTGCTTCAGTTGGACAGATTGTTATTATTGTCTCT  | 2929 |
| <br> |      |   |      |
| Qy   | 2986 | GCCCTGGC-AGAATGGCAGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACC   | 3044 |
|      |      |   |      |
| Db   | 2930 | GCCCTGGCTAGAATGGGGGCATAATCTGAGCCTTGTTCCCCTTGTCAGTGCGCTGACC  | 2989 |
| <br> |      |   |      |
| Qy   | 3045 | CCTTCACCTCTCCCCCTCCCTTTTTCTTTGTTTTGGGATTCAGAAAAC TGCTTGTCAGAG   | 3104 |
|      |      |   |      |
| Db   | 2990 | CTTGACCTCTT--CCTTCCTCCTCCCTTTGTTTGGGGATTCAGAAAAC TGCTTGTCACAG   | 3047 |
| <br> |      |   |      |
| Qy   | 3105 | ACTGTTTATTTTTTTATTAAAAAA  | 3126 |
|      |      |   |      |
| Db   | 3048 | ACAATTTATTTTTTTATTAAAAAA  | 3069 |

Query Match 43.7%; Score 1372.2; DB 9; Length 2172;  
Best Local Similarity 71.9%; Pred. No. 0;  
Matches 1560; Conservative 0; Mismatches 611; Indels 0; Gaps 0;

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Qy      105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
          ||||| ||| ||||| |||| | |||| |||| | ||| |||||
Db      1  ATGGCCCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTTCTTCCAA 60

Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 224
          || | | |||| | | | | | | | | | | |||||
Db      61 CTCTTCCTGCTGCCATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
          || |||| |||| |||| | | | | | |||| | |||||
Db      121 AGAGTCAAATACCATGCTGGAGACGGGCACAGGGCCCTCAGCTTCTTCCAACAAAAGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATCTCTCTACGTGGGGGCT 344
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Db      181 CTCCGAGACTTTGACACGCTGCTCCTGAGTGACGATGGCAACACTCTCTATGTGGGGGCT 240

Qy      345 CGAGAAGCCATTCTGGCCTTGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG 404
          |||| | | | ||||| ||||| | |||| | | |||||
Db      241 CGAGAGGCCGTCTTGGCCTTGAATATCCAGAACCAGGAATCCAAGGCTAAAGAACATG 300

Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
          |||| ||||| ||||| ||||| ||||| ||||| |||||
Db      301 ATACCCTGGCCAGCCAGTGAGAGAAAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCATCTCTAC 524
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Db      361 GAGACACAGTGTTCACCTTCATTCGAGTCTTGGTCTCTTACAATGCTACTCACCTCTAT 420

Qy      525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGACCTTCATTGAACCTCAAGATTCCCTAC 584
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Db      421 GCCTGTGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTGAACCTCAAGATTCCCTC 480

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          ||||| |||| | ||||| |||| | || ||||| |||||
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Qy      645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
          | ||||| || ||||| ||||| ||||| |||| | || |||||
Db      541 GTTCACAAGCACACAGCTGTCTTGGTCGATGGGATGCTTTATTCGGGCACCATGAACAAC 600

Qy      705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACC 764
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Db      601 TTCCTGGGCAGCGAGCCCATCCTGATGCGGACACTGGGATCCCAGCCTGTTCTCAAGACT 660

Qy      765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
          |||| |||| | |||||
Db      661 GACATCTTCTTACGCTGGCTGCACGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

Qy      825 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 884
Db      721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780

Qy      885 CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG 944
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[illegible]

Db 1621 GGCAACCCGGAGTGGGTATGCACCCGTGGCCCCATGGCCAGGAGCCCCCGGCGTCAGAGC 1680

Qy 1785 CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC 1844  
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Db 1681 CCCCCTCAACTAATTAAAGAAGTCCTGACAGTCCCCAACTCCATCCTGGAGCTGCCCTGC 1740

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Db 1741 CCCCACCTGTCAGCACTGGCCTCTTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAA 1800

Qy 1905 GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT 1964  
||||| | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1801 GCCTCTGCTACCGTCTACAATGGCTCCCTCTTGCTGCTGCCGCAGGATGGTGTGCGGGGC 1860

Qy 1965 CTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG 2024  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1861 CTCTACCACTGTGTGGCGACTGAGAACGGCTACTCATACCCTGTGGTCTCCTATTGGGTA 1920

Qy 2025 GACAGCCAGGACCAGACCCCTGGCCCTGGATCCTGAACCTGGCAGGCATCCCCGGGAGCAT 2084  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1921 GACAGCCAGGACCAGCCCCTGGCGCTGGACCCTGAGCTGGCGGGCGTTCCCCGTGAGCGT 1980

Qy 2085 GTGAAGGTCCCCTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC 2144  
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Db 1981 GTGCAGGTCCCCTGACCAGGGTCGGAGGCGGAGCTTCCATGGCTGCCCAGCGGTCTAC 2040

Qy 2145 TGGCCCCACTTTGTCACCTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC 2204  
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Db 2041 TGGCCCCATTTTCTCATCGTTACCGTCCTCCTGGCCATCGTGCTCCTGGGAGTGCTCACT 2100

Qy 2205 ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG 2264  
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Db 2101 CTCCTCCTCGCTTCCCCACTGGGGGCGCTGCGGGCTCGGGGTAAGGTTTCAGGGCTGTGGG 2160

Qy 2265 ACCCTGCGCCC 2275  
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Db 2161 ATGCTGCCCCC 2171

# RESULT 8

BX367242/c

LOCUS BX367242 1108 bp mRNA linear EST 27-APR-2004

DEFINITION BX367242 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
Homo sapiens cDNA clone CS0DL002Y004 3-PRIME, mRNA sequence.

ACCESSION BX367242

VERSION BX367242.2 GI:46625363

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1108)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30455608.  
Contact: Genoscope





|    |      |   |      |
|----|------|---|------|
| Db | 691  | CATGCTGGCTGGGCGGCCCAAGMACAGCCCTGACTAGGATSACAGCAGCACAAAAGACCA  | 632  |
| Qy | 2491 | CCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG  | 2550 |
|    |      | :     :   |      |
| Db | 631  | CCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATMACTGATVACACTCAGCAGGGTG  | 572  |
| Qy | 2551 | ATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAA  | 2610 |
|    |      |   |      |
| Db | 571  | ATGAACAGCAGTCTGCCTCCCCTATGGAACCTCCCTTCTACCAAGCACATGAGCTCTCTAA | 512  |
| Qy | 2611 | CAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGAT  | 2670 |
|    |      |   |      |
| Db | 511  | CAGGGTGGGGGCTACCCCCAGACCTGCTCCTAAACTGATATTGAAGAACCTGGAGAGGAT  | 452  |
| Qy | 2671 | CCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAA  | 2730 |
|    |      |   |      |
| Db | 451  | CCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAA  | 392  |
| Qy | 2731 | AAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGC  | 2790 |
|    |      | :   |      |
| Db | 391  | AAACCTGCMTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAAAAATAATATGC  | 332  |
| Qy | 2791 | TAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT  | 2850 |
|    |      | :                : :             :                            |      |
| Db | 331  | TAAMATGCAACTCCTGGAAACTCMAMTCTGAAGCTGCCGCTTTGAAMACCAAACACTCCCT | 272  |
| Qy | 2851 | TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCT  | 2910 |
|    |      | :   |      |
| Db | 271  | TCTCCCAGGGTCATGMAGGGATCTGCTCCCTCCTGCTTCCCTTACMAGTCGTGMACAGCT  | 212  |
| Qy | 2911 | GACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCCTTCTTGCTTCAGTTGGGGCAG | 2970 |
|    |      |   |      |
| Db | 211  | AACTCCCAGGAAGTCTTCCCTGAAGTCTGACCACCTTTCNTCTAGCTTAAGTTGGRGAAA  | 152  |
| Qy | 2971 | ACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTT  | 3030 |
|    |      |   |      |
| Db | 151  | ACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATNTGAGCCTTCTTAACTCCTT  | 92   |
| Qy | 3031 | TACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTTCAGAAA | 3090 |
|    |      |   |      |
| Db | 91   | TACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTTCAGAAA | 32   |
| Qy | 3091 | ACTGCTTGTTCAGAGACTGTTTATTTTTTTATT                             | 3121 |
|    |      |   |      |
| Db | 31   | ACTGCTTGTTCAGAGACTGTTTCBYTTTTTCTT                             | 1    |

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1064)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 5, 2003 this sequence version replaced gi:30384744.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 907.f  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?s=CS0DL005AB09NP1&c=907.f>.

FEATURES

source Location/Qualifiers

1. .1064  
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/mol\_type="mRNA"  
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/cell\_line="RAMOS CELL LINE"  
/clone\_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 29.5%; Score 926.2; DB 5; Length 1064;  
Best Local Similarity 95.5%; Pred. No. 1.2e-233;  
Matches 1000; Conservative 15; Mismatches 24; Indels 8; Gaps 6;

Qy 2058 GAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGG 2117  
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Db 1040 GATCTGAATGGCAGCATCCCCGGGAGMWGKGARGTCCCGTTGACC-RGGTCAGTGGTGGG 982

Qy 2118 GCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTT 2177  
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Db 981 --CCGCCCTGGYGCCAGCAGTCCWAYTG--CCCCATTTGTCACTGTCACTGTCTCTTT 926

Qy 2178 GCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGG 2237  
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Db 925 GCCTTAGTGCTTTCA-GAGCCCTCATCATCCTCGT-GCCTCCCCATTGAGAGCACTCCGG 868

Qy 2238 GCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGC 2297  
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Db 867 GCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGC 808

Qy 2298 AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT 2357  
||||||| ||||||||| ||||||||| |||||||||

|    |      |   |      |
|----|------|---|------|
| Db | 807  | AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT  | 748  |
| Qy | 2358 | GACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT | 2417 |
|    |      |   |      |
| Db | 747  | GACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT | 688  |
| Qy | 2418 | GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA  | 2477 |
|    |      |   |      |
| Db | 687  | GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA  | 628  |
| Qy | 2478 | GCACAAAAGACCACCTTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC | 2537 |
|    |      |   |      |
| Db | 627  | GCACAAAAGACCACCTTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC | 568  |
| Qy | 2538 | ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC  | 2597 |
|    |      |   |      |
| Db | 567  | ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC  | 508  |
| Qy | 2598 | ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA  | 2657 |
|    |      |   |      |
| Db | 507  | ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA  | 448  |
| Qy | 2658 | ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCTCCAGAAACACAGTGTTTC   | 2717 |
|    |      |   |      |
| Db | 447  | ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCTCCAGAAACACAGTGTTTC   | 388  |
| Qy | 2718 | AAGAGACCTTAAAAAACCTGCCTGTCCCAGGACCTTATGGTAATGAACACCAAACATCTA  | 2777 |
|    |      |   |      |
| Db | 387  | AAGAGACCTTAAAAAACCTGCCTGTCCCAGGACCTTATGGTAATGAACACCAAACATCTA  | 328  |
| Qy | 2778 | AACAATCATATGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTTGGAC   | 2837 |
|    |      |   |      |
| Db | 327  | AACAATCATATGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTTGGAC   | 268  |
| Qy | 2838 | ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA  | 2897 |
|    |      |   |      |
| Db | 267  | ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA  | 208  |
| Qy | 2898 | GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCCTGAAGTCTGACCACCTTCTTCTTGCT  | 2957 |
|    |      | :     :   |      |
| Db | 207  | GTCGTGCACCGCTGACTYCCAGGAAGTCTTCCCTGAAKTCTGACCACCTTCTTCTTGCT   | 148  |
| Qy | 2958 | TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG-CAGGGGTAATCTGAGC  | 3016 |
|    |      | : :     :   |      |
| Db | 147  | TCAGTTGGGGCAGAYTYTGATCCCTTCTGCCCTGGYAGAATGGTCAGGGGTAATCTGAGC  | 88   |
| Qy | 3017 | CTTCTTCACTCCTTTACCCTAGCTGACCCCTTACCTCTCCCCCTCCCTTTTCTTTGTT    | 3076 |
|    |      | : : :   |      |
| Db | 87   | CTTCTTCACTCCTTTACCCTAGCTGACCCCTTMCCTCTCCCCBTSSCTTTTCTTTGTT    | 28   |
| Qy | 3077 | TTGGGATTTCAGAAAACCTGCTTGTCAGA                                 | 3103 |
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| Db | 27   | TTGGGATTTCAGAAAACCTGCTTGTCAGA                                 | 1    |

LOCUS BX350606 922 bp mRNA linear EST 08-APR-2004  
 DEFINITION BX350606 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
 Homo sapiens cDNA clone CS0DL005YC17 3-PRIME, mRNA sequence.  
 ACCESSION BX350606  
 VERSION BX350606.1 GI:30373499  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 922)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 907.f  
 For more information about this cluster, see  
[http://www.genoscope.cns.fr/cdna?s=CS0BAI043ZD06\\_CS04076\\_1&c=907.f](http://www.genoscope.cns.fr/cdna?s=CS0BAI043ZD06_CS04076_1&c=907.f).  
 FEATURES  
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 25-NORMALIZED"  
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 primer. Five prime end enriched, double-strand cDNA was  
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 sites of the pCMVSPORT 6 vector. Library was normalized."  
 ORIGIN  
 Query Match 27.8%; Score 874.4; DB 5; Length 922;  
 Best Local Similarity 98.7%; Pred. No. 6.1e-220;  
 Matches 878; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
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 Db 919 CCCAGGNCCTTGATGGGCACAGCCATCTTGTCATGTACTTGGGAACCACAACAGGGTCGC 860  
 Qy 1432 TCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGGAAGAGATTTCAGCTGT 1491  
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 Db 859 TCCACAAGACTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGGAAGAGATTTCAGCTGT 800  
 Qy 1492 TCCCTGACCCTGAACCTGTTTCGAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTGTTG 1551  
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 Db 799 TCCCTGACCCTGANCTGTTTCGAACCTGCAGCTGGCCNCCACCAAGGGTGCAGTGTGTTG 740

|    |      |   |      |
|----|------|---|------|
| Qy | 1552 | TAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCT | 1611 |
|    |      |   |      |
| Db | 739  | TAGGCTTCTCAGNAGGTGTCTGGAGGGTGCNCCGAGCCAACCTGTAGTGTCTATGAGAGCT | 680  |
| Qy | 1612 | GTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCT  | 1671 |
|    |      |   |      |
| Db | 679  | GTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCT  | 620  |
| Qy | 1672 | GTTGCCTCCTGTCTGCCCCAACCTGAACCTCCTGGAAGCAGGACATGGAGCGGGGGAACC  | 1731 |
|    |      |   |      |
| Db | 619  | GTTGCCTCCTGTCTGCCCCAACCTGAACCTCCTGGAAGCAGGACATGGAGCGGGGGAACC  | 560  |
| Qy | 1732 | CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC  | 1791 |
|    |      |   |      |
| Db | 559  | CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC  | 500  |
| Qy | 1792 | AAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACC    | 1851 |
|    |      |   |      |
| Db | 499  | AAATCATTAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGCTCCCCTGCCCCACC    | 440  |
| Qy | 1852 | TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT  | 1911 |
|    |      |   |      |
| Db | 439  | TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT  | 380  |
| Qy | 1912 | CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC  | 1971 |
|    |      |   |      |
| Db | 379  | CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC  | 320  |
| Qy | 1972 | AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC  | 2031 |
|    |      |   |      |
| Db | 319  | AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC  | 260  |
| Qy | 2032 | AGGACCAGACCCTGGCCCTGGATCCTGAACCTGGCAGGCATCCCCCGGGAGCATGTGAAGG | 2091 |
|    |      |   |      |
| Db | 259  | AGGACCAGACCCTGGCCCTGGATCCTGAACCTGGCAGGCATCCCCCGGGAGCATGTGAAGG | 200  |
| Qy | 2092 | TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCC  | 2151 |
|    |      |   |      |
| Db | 199  | TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCC  | 140  |
| Qy | 2152 | ACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCG   | 2211 |
|    |      |   |      |
| Db | 139  | ACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCG   | 80   |
| Qy | 2212 | TGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGT           | 2261 |
|    |      |   |      |
| Db | 79   | TGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGT           | 30   |

# RESULT 11

BX384966

LOCUS BX384966 934 bp mRNA linear EST 23-APR-2004

DEFINITION BX384966 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.

ACCESSION BX384966

VERSION BX384966.2 GI:46556002

```

KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 934)
AUTHORS       Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE         Full-length cDNA libraries and normalization
JOURNAL       Unpublished (2001)
COMMENT       On May 8, 2003 this sequence version replaced gi:30436505.
               Contact: Genoscope
               Genoscope - Centre National de Sequencage
               2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
               end enriched, double-strand cDNA was digested with Not I and cloned
               into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
               was normalized. Library was constructed by Life Technologies, a
               division of Invitrogen. This sequence belongs to sequence cluster
               907.f
               For more information about this cluster, see
               http://www.genoscope.cns.fr/cdna?s=CS0DL005AB09QP1&c=907.f.
FEATURES
  source      Location/Qualifiers
               1. .934
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="CS0DL005YC17"
               /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
               /cell_line="RAMOS CELL LINE"
               /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
               25-NORMALIZED"
               /note="1st strand cDNA was primed with a NotI-oligo(dT)
               primer. Five prime end enriched, double-strand cDNA was
               digested with Not I and cloned into the Not I and EcoR V
               sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match      27.0%;  Score 849.2;  DB 5;  Length 934;
Best Local Similarity  97.0%;  Pred. No. 2.9e-213;
Matches 871;  Conservative 4;  Mismatches 22;  Indels 1;  Gaps 1;

Qy      99 CTGAGCATGGCCCTCCAGCCCTGGGCGCTGGACCCCTGGAGCCTCCTGGGCGCTTTTCCTC 158
      |||
Db      1 CTGAGCATGGCCCTCCAGCCCTGGGCGCTGGACCCCTGGAGCCTCCTGGGCGCTTTTCCTC 60

Qy      159 TTCCAAGTCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCC 218
      |||
Db      61 TTCCAAGTCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCC 120

Qy      219 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 278
      |||
Db      121 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 180

Qy      279 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG 338
      |||
Db      181 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG 240

```

|    |     |  |     |
|----|-----|--|-----|
| Qy | 339 | GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAG  | 398 |
|    |     |  |     |
| Db | 241 | GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAG  | 300 |
| Qy | 399 | AACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAG  | 458 |
|    |     |  |     |
| Db | 301 | AACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAG  | 360 |
| Qy | 459 | AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCAT   | 518 |
|    |     |  |     |
| Db | 361 | AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCAT   | 420 |
| Qy | 519 | CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT | 578 |
|    |     |  |     |
| Db | 421 | CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT | 480 |
| Qy | 579 | TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT | 638 |
|    |     |  |     |
| Db | 481 | TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT | 540 |
| Qy | 639 | GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG | 698 |
|    |     |  |     |
| Db | 541 | GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG | 600 |
| Qy | 699 | AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC | 758 |
|    |     |  |     |
| Db | 601 | AACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC | 660 |
| Qy | 759 | AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT | 818 |
|    |     |  |     |
| Db | 661 | AAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT | 720 |
| Qy | 819 | TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG | 878 |
|    |     |  |     |
| Db | 721 | TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG | 780 |
| Qy | 879 | AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG | 938 |
|    |     |  |     |
| Db | 781 | AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCG-AAARCTG | 839 |
| Qy | 939 | CTGCAGAAGAAGTGGACCACCTTCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGC     | 996 |
|    |     |  |     |
| Db | 840 | CTGCAGAAGAAGTGGACCMCTCCTGAAGCCCACYGCYCTCMCCAGCCCGGGCACTGC    | 897 |

# RESULT 12

BX328255

LOCUS BX328255 897 bp mRNA linear EST 07-APR-2004

DEFINITION BX328255 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.

ACCESSION BX328255

VERSION BX328255.2 GI:46262160

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





Qy 1104 AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA 1163  
 |||  
 Db 301 AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA 360

Qy 1164 TACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAAC 1223  
 |||  
 Db 361 TACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAAC 420

Qy 1224 CCCCAGGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG 1283  
 |||  
 Db 421 CCCCAGGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG 480

Qy 1284 GACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTG 1343  
 |||  
 Db 481 GACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTG 540

Qy 1344 GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC 1403  
 |||  
 Db 541 GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC 600

Qy 1404 ATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT 1463  
 |||  
 Db 601 ATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT 660

Qy 1464 GCTCATCTGGTGGGAAGAGATTGAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAG 1523  
 |||  
 Db 661 GCTCATCTGGTGGGAAGAGATTGAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAG 720

Qy 1524 CTGGCCCCCAGGGTGCA-GTGTGGTAGGCTTCTCAGGAGGTGTCTGG-AGGGTGC 1581  
 |||  
 Db 721 CTGGCCCCCAGGGTGCAAGTGTGGTAGGCTTCTCAGGAGGTGTCTGGNAGGGTGC 780

Qy 1582 CCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCC 1641  
 |||  
 Db 781 CCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCC 840

Qy 1642 ACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCT 1696  
 |||  
 Db 841 -CTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCT 894

RESULT 13

BQ057192

LOCUS BQ057192 974 bp mRNA linear EST 29-MAR-2002

DEFINITION AGENCOURT\_6769628 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5812383  
 5', mRNA sequence.

ACCESSION BQ057192

VERSION BQ057192.1 GI:19816532

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 974)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Lou Staudt  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2062 row: 1 column: 16  
High quality sequence stop: 714.

FEATURES Location/Qualifiers  
source 1. .974  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5812383"  
/tissue\_type="lymphoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_99"  
/note="Organ: lymph; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCACGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

# ORIGIN

Query Match 26.3%; Score 827.4; DB 5; Length 974;  
Best Local Similarity 92.6%; Pred. No. 1.8e-207;  
Matches 902; Conservative 0; Mismatches 67; Indels 5; Gaps 3;

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|----|-----|---|-----|
| Qy | 92  | TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCT  | 151 |
|    |     |   |     |
| Db | 1   | TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCT  | 60  |
| Qy | 152 | TTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCA | 211 |
|    |     |   |     |
| Db | 61  | TTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCA | 120 |
| Qy | 212 | GGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT  | 271 |
|    |     |   |     |
| Db | 121 | GGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT  | 180 |
| Qy | 272 | CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT  | 331 |
|    |     |   |     |
| Db | 181 | CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT  | 240 |
| Qy | 332 | CTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG  | 391 |
|    |     |   |     |
| Db | 241 | CTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG  | 300 |
| Qy | 392 | GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAA  | 451 |

|    |      |  |   |      |
|----|------|--|---|------|
| Db | 301  |  | GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAA  | 360  |
| Qy | 452  |  | GAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGT  | 511  |
| Db | 361  |  | GAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGT  | 420  |
| Qy | 512  |  | CACCCATCTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCTTCATTGAACT | 571  |
| Db | 421  |  | CACCCATCTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCTTCATTGAACT | 480  |
| Qy | 572  |  | TCAAGATTCTTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG  | 631  |
| Db | 481  |  | TCAAGATTCTTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG  | 540  |
| Qy | 632  |  | CCCCTTTGACCCCGCTCACAAGCATACGGCTGCTTGGTGGATGGGATGCTCTATTCTGG   | 691  |
| Db | 541  |  | CCCCTTTGACCCCGCTCACAAGCATACGGCTGCTTGGTGGATGGGATGCTCTATTCTGG   | 600  |
| Qy | 692  |  | TACTATGAACAACCTTCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCC  | 751  |
| Db | 601  |  | TACTATGAACAACCTTCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCC  | 660  |
| Qy | 752  |  | TGTCCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC  | 811  |
| Db | 661  |  | TGTCCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC  | 720  |
| Qy | 812  |  | CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTT  | 871  |
| Db | 721  |  | CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGGAGAGACAGCCAGCGAGTTTGACTT  | 780  |
| Qy | 872  |  | CTTTGAGAGGCTCCACACATCGCGGGTGG-CTAGAGTCTGCAAGAATGACGTGGGC-GGC  | 929  |
| Db | 781  |  | CTTTGAGAGGCCCCACCTCCCGGGGGCCTANAGTCTGCCAAAATGACGTGGGCGGGC     | 840  |
| Qy | 930  |  | GAAAAGCTGCTGCAGAAGAA---GTGGACCACCTTCTTGAAGGCCAGCTGCTCTGCACC   | 986  |
| Db | 841  |  | GAAAAGCTGCTGCAAAAAAAGTGGACCCCCCTTCTTGAAGGCCAGCTGCTCTGGCCC     | 900  |
| Qy | 987  |  | CAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCT   | 1046 |
| Db | 901  |  | CCAGCCGGGGGAGCTTGCCCTTTCACGTCATTCGCCGCCCGGGTCTTGGCTCCCCC      | 960  |
| Qy | 1047 |  | CCCACAGCTCCCCA  | 1060 |
| Db | 961  |  | CCGAATTTTCCCCA  | 974  |

RESULT 14

BX390196

LOCUS BX390196 944 bp mRNA linear EST 29-APR-2004

DEFINITION BX390196 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CS0DD003YE08 5-PRIME, mRNA sequence.

ACCESSION BX390196

VERSION BX390196.2 GI:46873199

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 944)

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30463276.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 907.f  
 For more information about this cluster, see  
[http://www.genoscope.cns.fr/cdna?s=CS0BAG009ZD12\\_CS00860\\_1&c=907.f](http://www.genoscope.cns.fr/cdna?s=CS0BAG009ZD12_CS00860_1&c=907.f).

FEATURES Location/Qualifiers

source 1. .944  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DD003YE08"  
 /tissue\_type="NEUROBLASTOMA COT 50-NORMALIZED"  
 /clone\_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

# ORIGIN

Query Match 26.1%; Score 820.4; DB 5; Length 944;  
 Best Local Similarity 97.4%; Pred. No. 1.3e-205;  
 Matches 897; Conservative 0; Mismatches 17; Indels 7; Gaps 6;

Qy 1535 CCAGGGTGCAGTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTG 1594  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 CCAGGGTGCAGTGTGTTGTAGGCTTCT-AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTG 59

Qy 1595 TAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGA 1654  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 60 TAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGA 119

Qy 1655 CCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGA 1714  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 120 CCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGA 179

Qy 1715 CATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCG 1774  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 180 CATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCG 239

Qy 1775 GCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGA 1834  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 240 GCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGA 299

|    |      |   |      |
|----|------|---|------|
| Qy | 1835 | GCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGC   | 1894 |
|    |      |   |      |
| Db | 300  | GCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGC   | 359  |
| Qy | 1895 | AGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGG  | 1954 |
|    |      |   |      |
| Db | 360  | AGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGG  | 419  |
| Qy | 1955 | AGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTC  | 2014 |
|    |      |   |      |
| Db | 420  | AGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTC  | 479  |
| Qy | 2015 | CTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCC  | 2074 |
|    |      |   |      |
| Db | 480  | CTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCC  | 539  |
| Qy | 2075 | CCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCCA | 2134 |
|    |      |   |      |
| Db | 540  | CCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCCA | 599  |
| Qy | 2135 | GCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTTCAGG  | 2194 |
|    |      |   |      |
| Db | 600  | GCAGTCCTACTGGCCCCACTNTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTTCAGG  | 659  |
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| Db | 660  | AGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTTCGGGCAAGGTTCA  | 719  |
| Qy | 2254 | AGGGCTGTGAGACCCTGCGCCCTGGGG--AGAAGGCCCGTTAAGCAGAGAGCAACA-CC   | 2310 |
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| Db | 720  | AGGGCTGTGAGACCCTGCGCCCTGGGGGAGAAGGGCCCGTTAAGCAGAGAGCAACACCC   | 779  |
| Qy | 2311 | TCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACG-CTGACAACAACCTGC | 2369 |
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| Qy | 2370 | CTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGG  | 2429 |
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| Qy | 2430 | CCATGCTGGCTGGGCGGCCCA   | 2450 |
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RESULT 15

CB243787/c

LOCUS CB243787 797 bp mRNA linear EST 12-FEB-2003

DEFINITION UI-CF-FN0-agg-a-05-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone  
UI-CF-FN0-agg-a-05-0-UI 3', mRNA sequence.

ACCESSION CB243787

VERSION CB243787.1 GI:28365431

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 797)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

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 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
 The following repetitive elements were found in this cDNA sequence: 1-46, >AT\_rich#Low\_complexity (matched compliment)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES Location/Qualifiers

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 /mol\_type="mRNA"  
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 /tissue\_type="Human Lung Epithelial cells"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-CF-FN0"  
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-CF-FN0 is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu  
 TAG\_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h  
 TAG\_LIB=UI-CF-FN0  
 TAG\_SEQ=CTGCTCAGGT"

#### ORIGIN

Query Match 24.8%; Score 779.8; DB 6; Length 797;  
 Best Local Similarity 99.4%; Pred. No. 7e-195;  
 Matches 781; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 Db 797 GACAACAAGTGCNTAGGCACTGAGGTAGCTTAAACTNTAGGCACAGGCCGGGGCTGCGGT 738

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| Qy | 2898 | GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCT    | 2957 |
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Job time : 9877 secs



OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 19:11:26 ; Search time 1686 Seconds  
(without alignments)  
10999.493 Million cell updates/sec

Title: US-10-015-391A-276  
Perfect score: 3143  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 74     | 2476.4 | 78.8        | 2768   | 17 | US-10-470-360-35     | Sequence 35, Appl |  |
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| 85     | 1727.6 | 55.0        | 3046   | 13 | US-10-042-431-71     | Sequence 71, Appl |  |
| 86     | 1727.6 | 55.0        | 3046   | 13 | US-10-042-431-77     | Sequence 77, Appl |  |
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| c 89   | 576    | 18.3        | 576    | 16 | US-10-029-386-25944  | Sequence 25944, A |  |
| 90     | 551    | 17.5        | 551    | 9  | US-09-796-692-9413   | Sequence 9413, Ap |  |
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| 104    | 327.8  | 10.4        | 400    | 17 | US-10-085-783A-11273 | Sequence 11273, A |  |
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| 697    | 255.6  | 8.1         | 3766   | 17 | US-10-085-117-71     | Sequence 71, Appl |  |
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| 699    | 237.8  | 7.6         | 3293   | 14 | US-10-149-819-25     | Sequence 25, Appl |  |

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| 701   | 236.6 | 7.5 | 2155 | 14 | US-10-002-050-11     | Sequence 11, Appl |
| 702   | 236.6 | 7.5 | 2155 | 14 | US-10-002-304-11     | Sequence 11, Appl |
| 703   | 236.6 | 7.5 | 2156 | 13 | US-10-003-152-21     | Sequence 21, Appl |
| 704   | 236.6 | 7.5 | 2156 | 14 | US-10-002-050-21     | Sequence 21, Appl |
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| 706   | 236.6 | 7.5 | 2284 | 13 | US-10-003-152-13     | Sequence 13, Appl |
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| 709   | 236.6 | 7.5 | 2646 | 17 | US-10-312-352-67     | Sequence 67, Appl |
| 710   | 235   | 7.5 | 238  | 9  | US-09-796-692-2787   | Sequence 2787, Ap |
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| 720   | 235   | 7.5 | 1914 | 17 | US-10-403-676-7      | Sequence 7, Appli |
| 721   | 235   | 7.5 | 1914 | 17 | US-10-403-676-9      | Sequence 9, Appli |
| 722   | 235   | 7.5 | 3503 | 10 | US-09-759-130B-336   | Sequence 336, App |
| 723   | 235   | 7.5 | 3503 | 14 | US-10-189-123-66     | Sequence 66, Appl |
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| 725   | 235   | 7.5 | 3503 | 18 | US-10-741-790-336    | Sequence 336, App |
| 726   | 233.2 | 7.4 | 2739 | 17 | US-10-403-676-11     | Sequence 11, Appl |
| 727   | 233.2 | 7.4 | 3868 | 17 | US-10-190-115-13     | Sequence 13, Appl |
| 728   | 233.2 | 7.4 | 3868 | 17 | US-10-369-072-13     | Sequence 13, Appl |
| 729   | 230   | 7.3 | 2433 | 17 | US-10-291-808-24     | Sequence 24, Appl |
| 730   | 225.4 | 7.2 | 2558 | 17 | US-10-190-115-15     | Sequence 15, Appl |
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| 732   | 225.4 | 7.2 | 3112 | 17 | US-10-190-115-17     | Sequence 17, Appl |
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| 737   | 200.8 | 6.4 | 3360 | 18 | US-10-115-635-8      | Sequence 8, Appli |
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| 739   | 189.6 | 6.0 | 8095 | 9  | US-09-989-920-73     | Sequence 73, Appl |
| 740   | 189.6 | 6.0 | 8144 | 11 | US-09-989-890-112    | Sequence 112, App |
| c 741 | 177.2 | 5.6 | 1662 | 13 | US-10-027-632-97791  | Sequence 97791, A |
| c 742 | 177.2 | 5.6 | 1662 | 13 | US-10-027-632-100416 | Sequence 100416,  |
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| 747   | 169.8 | 5.4 | 2562 | 17 | US-10-085-117-68     | Sequence 68, Appl |
| 748   | 169.8 | 5.4 | 2562 | 17 | US-10-085-117-69     | Sequence 69, Appl |
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| 757   | 147   | 4.7 | 1024 | 17 | US-10-042-865-3    | Sequence 3, Appli |
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| 759   | 143.6 | 4.6 | 2769 | 17 | US-10-052-482-164  | Sequence 164, App |
| 760   | 141   | 4.5 | 967  | 13 | US-10-000-512-11   | Sequence 11, Appl |
| 761   | 141   | 4.5 | 967  | 17 | US-10-074-566-11   | Sequence 11, Appl |
| 762   | 126   | 4.0 | 1801 | 17 | US-10-211-462-164  | Sequence 164, App |
| 763   | 126   | 4.0 | 3524 | 16 | US-10-391-413-3    | Sequence 3, Appli |
| 764   | 126   | 4.0 | 3524 | 17 | US-10-211-462-166  | Sequence 166, App |
| 783   | 126   | 4.0 | 3721 | 14 | US-10-036-160-34   | Sequence 34, Appl |
| 913   | 126   | 4.0 | 3721 | 15 | US-10-223-085-267  | Sequence 267, App |
| 916   | 126   | 4.0 | 3721 | 15 | US-10-223-084-267  | Sequence 267, App |
| 917   | 126   | 4.0 | 3721 | 15 | US-10-223-088-267  | Sequence 267, App |
| 918   | 126   | 4.0 | 3721 | 15 | US-10-223-090-267  | Sequence 267, App |
| 919   | 126   | 4.0 | 3721 | 15 | US-10-223-087-267  | Sequence 267, App |
| 921   | 126   | 4.0 | 3721 | 15 | US-10-223-083-267  | Sequence 267, App |
| 922   | 126   | 4.0 | 3721 | 15 | US-10-223-089-267  | Sequence 267, App |
| 1083  | 126   | 4.0 | 3721 | 16 | US-10-223-081-267  | Sequence 267, App |
| 1099  | 126   | 4.0 | 3721 | 16 | US-10-223-082-267  | Sequence 267, App |
| 1210  | 126   | 4.0 | 3721 | 17 | US-10-305-654-267  | Sequence 267, App |
| 1219  | 126   | 4.0 | 3721 | 17 | US-10-081-056-267  | Sequence 267, App |
| 1232  | 126   | 4.0 | 3721 | 18 | US-10-884-091-34   | Sequence 34, Appl |
| 1233  | 126   | 4.0 | 3721 | 19 | US-10-931-886-543  | Sequence 543, App |
| 1234  | 125.4 | 4.0 | 3692 | 16 | US-10-391-413-1    | Sequence 1, Appli |
| 1235  | 121.8 | 3.9 | 3279 | 15 | US-10-102-524-1855 | Sequence 1855, Ap |
| 1236  | 121.8 | 3.9 | 3453 | 15 | US-10-102-524-1854 | Sequence 1854, Ap |
| 1237  | 121.8 | 3.9 | 3606 | 15 | US-10-102-524-1853 | Sequence 1853, Ap |
| 1238  | 121.8 | 3.9 | 3631 | 17 | US-10-190-115-107  | Sequence 107, App |
| 1239  | 121.8 | 3.9 | 3791 | 18 | US-10-775-920-310  | Sequence 310, App |
| 1240  | 121.8 | 3.9 | 4233 | 17 | US-10-190-115-105  | Sequence 105, App |
| 1241  | 121.8 | 3.9 | 4456 | 17 | US-10-451-010-15   | Sequence 15, Appl |
| 1242  | 121.8 | 3.9 | 4559 | 15 | US-10-102-524-1852 | Sequence 1852, Ap |
| 1243  | 121.8 | 3.9 | 4559 | 18 | US-10-775-920-308  | Sequence 308, App |
| 1252  | 121.8 | 3.9 | 4725 | 14 | US-10-237-535-95   | Sequence 95, Appl |
| 1261  | 121.8 | 3.9 | 4725 | 14 | US-10-239-196-95   | Sequence 95, Appl |
| 1352  | 121.8 | 3.9 | 4725 | 18 | US-10-643-795A-55  | Sequence 55, Appl |
| 1353  | 121.8 | 3.9 | 6408 | 17 | US-10-190-115-11   | Sequence 11, Appl |
| 1354  | 121.8 | 3.9 | 6408 | 17 | US-10-369-072-11   | Sequence 11, Appl |
| 1355  | 121.4 | 3.9 | 2820 | 9  | US-09-854-845-15   | Sequence 15, Appl |
| 1356  | 121.4 | 3.9 | 2865 | 9  | US-09-854-845-13   | Sequence 13, Appl |
| 1357  | 121.4 | 3.9 | 3105 | 9  | US-09-854-845-5    | Sequence 5, Appli |
| 1358  | 121.4 | 3.9 | 3150 | 9  | US-09-854-845-1    | Sequence 1, Appli |
| 1359  | 121.4 | 3.9 | 3237 | 9  | US-09-854-845-7    | Sequence 7, Appli |
| 1360  | 121.4 | 3.9 | 3282 | 9  | US-09-854-845-3    | Sequence 3, Appli |
| 1361  | 121.4 | 3.9 | 3411 | 9  | US-09-854-845-11   | Sequence 11, Appl |
| 1362  | 121.4 | 3.9 | 3456 | 9  | US-09-854-845-9    | Sequence 9, Appli |
| 1363  | 121.4 | 3.9 | 4074 | 9  | US-09-854-845-17   | Sequence 17, Appl |
| 1364  | 115.6 | 3.7 | 2811 | 10 | US-09-759-130B-303 | Sequence 303, App |
| 1365  | 115.6 | 3.7 | 2811 | 14 | US-10-189-123-33   | Sequence 33, Appl |
| 1366  | 115.6 | 3.7 | 2811 | 16 | US-10-188-495-33   | Sequence 33, Appl |
| 1367  | 115.6 | 3.7 | 2811 | 18 | US-10-741-790-303  | Sequence 303, App |
| 1368  | 114.4 | 3.6 | 2675 | 18 | US-10-367-094-91   | Sequence 91, Appl |
| c1369 | 110   | 3.5 | 344  | 9  | US-09-917-800A-651 | Sequence 651, App |
| 1370  | 105.4 | 3.4 | 2094 | 9  | US-09-854-845-24   | Sequence 24, Appl |
| 1371  | 105.4 | 3.4 | 2517 | 9  | US-09-854-845-28   | Sequence 28, Appl |
| 1372  | 105.4 | 3.4 | 2598 | 9  | US-09-854-845-32   | Sequence 32, Appl |
| 1373  | 105.4 | 3.4 | 2951 | 9  | US-09-854-845-50   | Sequence 50, Appl |
| 1374  | 102.8 | 3.3 | 2337 | 9  | US-09-731-179-3    | Sequence 3, Appli |

|      |       |     |      |    |                    |                   |
|------|-------|-----|------|----|--------------------|-------------------|
| 1375 | 102.4 | 3.3 | 2109 | 9  | US-09-854-845-22   | Sequence 22, Appl |
| 1376 | 102.4 | 3.3 | 2532 | 9  | US-09-854-845-26   | Sequence 26, Appl |
| 1377 | 102.4 | 3.3 | 2575 | 17 | US-10-120-988-40   | Sequence 40, Appl |
| 1378 | 102.4 | 3.3 | 2613 | 9  | US-09-854-845-30   | Sequence 30, Appl |
| 1379 | 102   | 3.2 | 1327 | 17 | US-10-449-548-21   | Sequence 21, Appl |
| 1380 | 102   | 3.2 | 1327 | 17 | US-10-403-676-21   | Sequence 21, Appl |
| 1381 | 102   | 3.2 | 1492 | 17 | US-10-449-548-23   | Sequence 23, Appl |
| 1382 | 102   | 3.2 | 1492 | 17 | US-10-403-676-23   | Sequence 23, Appl |
| 1383 | 102   | 3.2 | 1878 | 17 | US-10-449-548-33   | Sequence 33, Appl |
| 1384 | 102   | 3.2 | 1878 | 17 | US-10-403-676-33   | Sequence 33, Appl |
| 1385 | 102   | 3.2 | 1890 | 10 | US-09-991-053-29   | Sequence 29, Appl |
| 1386 | 102   | 3.2 | 1890 | 10 | US-09-957-187-29   | Sequence 29, Appl |
| 1387 | 102   | 3.2 | 1890 | 10 | US-09-957-187-82   | Sequence 82, Appl |
| 1388 | 102   | 3.2 | 1908 | 17 | US-10-449-548-35   | Sequence 35, Appl |
| 1389 | 102   | 3.2 | 1908 | 17 | US-10-403-676-35   | Sequence 35, Appl |
| 1390 | 102   | 3.2 | 1921 | 17 | US-10-449-548-15   | Sequence 15, Appl |
| 1391 | 102   | 3.2 | 1921 | 17 | US-10-403-676-15   | Sequence 15, Appl |
| 1392 | 102   | 3.2 | 1948 | 17 | US-10-449-548-49   | Sequence 49, Appl |
| 1393 | 102   | 3.2 | 1948 | 17 | US-10-403-676-49   | Sequence 49, Appl |
| 1394 | 102   | 3.2 | 2583 | 17 | US-10-449-548-51   | Sequence 51, Appl |
| 1395 | 102   | 3.2 | 2583 | 17 | US-10-403-676-51   | Sequence 51, Appl |
| 1396 | 102   | 3.2 | 2634 | 17 | US-10-449-548-53   | Sequence 53, Appl |
| 1397 | 102   | 3.2 | 2634 | 17 | US-10-403-676-53   | Sequence 53, Appl |
| 1398 | 102   | 3.2 | 2944 | 17 | US-10-449-548-29   | Sequence 29, Appl |
| 1399 | 102   | 3.2 | 2944 | 17 | US-10-403-676-29   | Sequence 29, Appl |
| 1400 | 102   | 3.2 | 2995 | 17 | US-10-449-548-19   | Sequence 19, Appl |
| 1401 | 102   | 3.2 | 2995 | 17 | US-10-403-676-19   | Sequence 19, Appl |
| 1402 | 102   | 3.2 | 3055 | 17 | US-10-449-548-27   | Sequence 27, Appl |
| 1403 | 102   | 3.2 | 3055 | 17 | US-10-403-676-27   | Sequence 27, Appl |
| 1404 | 102   | 3.2 | 3106 | 17 | US-10-449-548-17   | Sequence 17, Appl |
| 1405 | 102   | 3.2 | 3106 | 17 | US-10-403-676-17   | Sequence 17, Appl |
| 1406 | 102   | 3.2 | 3165 | 17 | US-10-449-548-47   | Sequence 47, Appl |
| 1407 | 102   | 3.2 | 3165 | 17 | US-10-403-676-47   | Sequence 47, Appl |
| 1408 | 102   | 3.2 | 3333 | 10 | US-09-991-053-5    | Sequence 5, Appli |
| 1409 | 102   | 3.2 | 3333 | 10 | US-09-957-187-5    | Sequence 5, Appli |
| 1410 | 102   | 3.2 | 3498 | 10 | US-09-991-053-3    | Sequence 3, Appli |
| 1411 | 102   | 3.2 | 3498 | 10 | US-09-957-187-3    | Sequence 3, Appli |
| 1412 | 102   | 3.2 | 3498 | 17 | US-10-449-548-31   | Sequence 31, Appl |
| 1413 | 102   | 3.2 | 3498 | 17 | US-10-403-676-31   | Sequence 31, Appl |
| 1414 | 102   | 3.2 | 4250 | 10 | US-09-957-187-84   | Sequence 84, Appl |
| 1415 | 102   | 3.2 | 4250 | 16 | US-10-393-892-30   | Sequence 30, Appl |
| 1416 | 102   | 3.2 | 4250 | 16 | US-10-394-382-30   | Sequence 30, Appl |
| 1417 | 102   | 3.2 | 4250 | 17 | US-10-449-548-13   | Sequence 13, Appl |
| 1418 | 102   | 3.2 | 4250 | 17 | US-10-403-676-13   | Sequence 13, Appl |
| 1419 | 102   | 3.2 | 4250 | 18 | US-10-723-860-2800 | Sequence 2800, Ap |
| 1420 | 102   | 3.2 | 4280 | 17 | US-10-120-988-330  | Sequence 330, App |
| 1421 | 102   | 3.2 | 4612 | 18 | US-10-367-094-94   | Sequence 94, Appl |
| 1422 | 102   | 3.2 | 7281 | 18 | US-10-723-860-5596 | Sequence 5596, Ap |
| 1423 | 100.4 | 3.2 | 1438 | 17 | US-10-449-548-25   | Sequence 25, Appl |
| 1424 | 100.4 | 3.2 | 1438 | 17 | US-10-403-676-25   | Sequence 25, Appl |
| 1425 | 100.4 | 3.2 | 2113 | 17 | US-10-449-548-55   | Sequence 55, Appl |
| 1426 | 100.4 | 3.2 | 2113 | 17 | US-10-403-676-55   | Sequence 55, Appl |
| 1427 | 100.4 | 3.2 | 3983 | 17 | US-10-449-548-45   | Sequence 45, Appl |
| 1428 | 100.4 | 3.2 | 3983 | 17 | US-10-403-676-45   | Sequence 45, Appl |
| 1429 | 99    | 3.1 | 2893 | 10 | US-09-808-665A-1   | Sequence 1, Appli |
| 1430 | 99    | 3.1 | 2894 | 10 | US-09-808-665A-3   | Sequence 3, Appli |
| 1431 | 98.6  | 3.1 | 1797 | 9  | US-09-854-845-40   | Sequence 40, Appl |

|      |      |     |      |    |                    |                   |
|------|------|-----|------|----|--------------------|-------------------|
| 1432 | 98.6 | 3.1 | 2220 | 9  | US-09-854-845-44   | Sequence 44, Appl |
| 1433 | 98.6 | 3.1 | 2301 | 9  | US-09-854-845-48   | Sequence 48, Appl |
| 1434 | 98.6 | 3.1 | 2790 | 14 | US-10-300-834-5    | Sequence 5, Appli |
| 1435 | 98.6 | 3.1 | 3432 | 14 | US-10-300-834-4    | Sequence 4, Appli |
| 1436 | 95.6 | 3.0 | 1812 | 9  | US-09-854-845-38   | Sequence 38, Appl |
| 1437 | 95.6 | 3.0 | 2235 | 9  | US-09-854-845-42   | Sequence 42, Appl |
| 1438 | 95.6 | 3.0 | 2316 | 9  | US-09-854-845-46   | Sequence 46, Appl |
| 1439 | 92.8 | 3.0 | 729  | 10 | US-09-759-130B-304 | Sequence 304, App |
| 1440 | 92.8 | 3.0 | 729  | 14 | US-10-189-123-34   | Sequence 34, Appl |
| 1441 | 92.8 | 3.0 | 729  | 16 | US-10-188-495-34   | Sequence 34, Appl |
| 1442 | 92.8 | 3.0 | 729  | 18 | US-10-741-790-304  | Sequence 304, App |
| 1443 | 89.8 | 2.9 | 2787 | 14 | US-10-300-834-2    | Sequence 2, Appli |
| 1444 | 89.8 | 2.9 | 3195 | 14 | US-10-300-834-1    | Sequence 1, Appli |
| 1445 | 89.4 | 2.8 | 4003 | 18 | US-10-723-860-5060 | Sequence 5060, Ap |
| 1446 | 83   | 2.6 | 2919 | 15 | US-10-262-538-11   | Sequence 11, Appl |
| 1447 | 83   | 2.6 | 2919 | 16 | US-10-285-351B-2   | Sequence 2, Appli |
| 1448 | 83   | 2.6 | 2919 | 18 | US-10-669-176-11   | Sequence 11, Appl |
| 1449 | 79.6 | 2.5 | 2349 | 9  | US-09-813-290-3    | Sequence 3, Appli |
| 1450 | 79.6 | 2.5 | 2628 | 9  | US-09-813-290-1    | Sequence 1, Appli |
| 1451 | 79.6 | 2.5 | 3568 | 9  | US-09-813-290-5    | Sequence 5, Appli |
| 1452 | 79.6 | 2.5 | 4700 | 17 | US-10-172-118-1824 | Sequence 1824, Ap |
| 1453 | 79.6 | 2.5 | 4700 | 17 | US-10-342-887-1824 | Sequence 1824, Ap |
| 1454 | 79.6 | 2.5 | 4700 | 18 | US-10-723-860-2944 | Sequence 2944, Ap |
| 1455 | 79.6 | 2.5 | 4936 | 18 | US-10-723-860-6994 | Sequence 6994, Ap |
| 1456 | 78.6 | 2.5 | 3560 | 16 | US-10-067-632-59   | Sequence 59, Appl |
| 1457 | 78.2 | 2.5 | 1923 | 18 | US-10-312-281-12   | Sequence 12, Appl |
| 1458 | 78.2 | 2.5 | 1923 | 18 | US-10-461-791-12   | Sequence 12, Appl |
| 1459 | 78.2 | 2.5 | 3261 | 18 | US-10-312-281-5    | Sequence 5, Appli |
| 1460 | 78.2 | 2.5 | 3261 | 18 | US-10-461-791-5    | Sequence 5, Appli |
| 1461 | 78.2 | 2.5 | 3694 | 18 | US-10-312-281-3    | Sequence 3, Appli |
| 1462 | 78.2 | 2.5 | 3694 | 18 | US-10-461-791-3    | Sequence 3, Appli |
| 1463 | 78   | 2.5 | 1491 | 9  | US-09-854-845-20   | Sequence 20, Appl |
| 1464 | 76.6 | 2.4 | 1896 | 17 | US-10-016-248-9    | Sequence 9, Appli |
| 1465 | 76.6 | 2.4 | 2191 | 17 | US-10-016-248-13   | Sequence 13, Appl |
| 1466 | 76.6 | 2.4 | 2359 | 17 | US-10-016-248-17   | Sequence 17, Appl |
| 1467 | 76.6 | 2.4 | 3196 | 17 | US-10-016-248-15   | Sequence 15, Appl |
| 1468 | 76.6 | 2.4 | 3205 | 17 | US-10-016-248-11   | Sequence 11, Appl |
| 1469 | 76.6 | 2.4 | 3364 | 17 | US-10-016-248-19   | Sequence 19, Appl |
| 1470 | 76.6 | 2.4 | 4234 | 17 | US-10-451-010-12   | Sequence 12, Appl |
| 1471 | 76.2 | 2.4 | 2340 | 9  | US-09-731-179-1    | Sequence 1, Appli |
| 1472 | 71.4 | 2.3 | 8056 | 18 | US-10-723-860-4273 | Sequence 4273, Ap |
| 1473 | 71.4 | 2.3 | 8214 | 18 | US-10-723-860-8119 | Sequence 8119, Ap |
| 1474 | 71.2 | 2.3 | 928  | 14 | US-10-188-246-13   | Sequence 13, Appl |
| 1475 | 71.2 | 2.3 | 1194 | 9  | US-09-854-845-36   | Sequence 36, Appl |
| 1476 | 69.8 | 2.2 | 2670 | 16 | US-10-067-632-61   | Sequence 61, Appl |
| 1477 | 68   | 2.2 | 777  | 14 | US-10-188-246-15   | Sequence 15, Appl |
| 1478 | 66.6 | 2.1 | 1755 | 9  | US-09-978-249-4    | Sequence 4, Appli |
| 1479 | 65.2 | 2.1 | 648  | 9  | US-09-854-845-18   | Sequence 18, Appl |
| 1480 | 63.8 | 2.0 | 2530 | 14 | US-10-097-340-283  | Sequence 283, App |
| 1481 | 63.8 | 2.0 | 2530 | 15 | US-10-262-538-9    | Sequence 9, Appli |
| 1482 | 63.8 | 2.0 | 2530 | 18 | US-10-669-176-9    | Sequence 9, Appli |
| 1483 | 63.8 | 2.0 | 2530 | 18 | US-10-723-860-2569 | Sequence 2569, Ap |
| 1484 | 63.8 | 2.0 | 2601 | 16 | US-10-067-632-53   | Sequence 53, Appl |
| 1485 | 63.8 | 2.0 | 2709 | 9  | US-09-774-490-1    | Sequence 1, Appli |
| 1486 | 63.8 | 2.0 | 2848 | 16 | US-10-247-671-83   | Sequence 83, Appl |
| 1487 | 63.8 | 2.0 | 3023 | 18 | US-10-723-860-6714 | Sequence 6714, Ap |
| 1488 | 62   | 2.0 | 2854 | 16 | US-10-067-632-57   | Sequence 57, Appl |

|       |      |     |       |    |                     |                   |
|-------|------|-----|-------|----|---------------------|-------------------|
| c1489 | 60.6 | 1.9 | 828   | 17 | US-10-276-774-37    | Sequence 37, Appl |
| 1490  | 60   | 1.9 | 60    | 10 | US-09-908-975-15844 | Sequence 15844, A |
| 1491  | 58.4 | 1.9 | 351   | 9  | US-09-854-845-34    | Sequence 34, Appl |
| 1492  | 58   | 1.8 | 39780 | 17 | US-10-052-482-163   | Sequence 163, App |
| 1493  | 57.6 | 1.8 | 3552  | 17 | US-10-231-956A-437  | Sequence 437, App |
| 1494  | 57.6 | 1.8 | 3552  | 18 | US-10-775-169-25    | Sequence 25, Appl |
| 1495  | 57.2 | 1.8 | 495   | 10 | US-09-918-995-51    | Sequence 51, Appl |
| 1496  | 56.6 | 1.8 | 48244 | 17 | US-10-052-482-166   | Sequence 166, App |
| 1497  | 55.6 | 1.8 | 273   | 11 | US-09-864-408A-5889 | Sequence 5889, Ap |
| 1498  | 53   | 1.7 | 64921 | 17 | US-10-085-117-70    | Sequence 70, Appl |
| 1499  | 52.6 | 1.7 | 2898  | 13 | US-10-144-031-2     | Sequence 2, Appli |
| 1500  | 52.4 | 1.7 | 445   | 9  | US-09-764-853-385   | Sequence 385, App |

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